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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-15

Perfect score: 11

Sequence: 1 ASQAKRRKGPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Query Score	Match	Length	DB	ID	Description
1	11	100.0	11	3	AAY88543	Aay88543 NCAM Ig1
2	11	100.0	11	5	ABG69343	Abg69343 Human neu
3	4	36.4	11	1	AAP82563	Aap82563 HTLV-III
4	4	36.4	11	2	AAR37408	Aar37408 Factor X-
5	4	36.4	11	2	AAY04449	Aay04449 Myelin ba
6	4	36.4	11	2	AAR93572	Aar93572 Dopamine
7	4	36.4	11	2	AAW69570	Aaw69570 Factor X
8	4	36.4	11	2	AAW39791	Aaw39791 Tobacco P
9	4	36.4	11	2	AAY43551	Aay43551 Peptide d

10	4	36.4	11	2	AAY23947	Aay23947 Peptide w
11	4	36.4	11	3	AAY51590	Aay51590 HIV-1 der
12	4	36.4	11	3	AAY67514	Aay67514 Factor X-
13	4	36.4	11	3	AAB14107	Aab14107 HLA DR B3
14	4	36.4	11	3	AAB14105	Aab14105 HLA DR B3
15	4	36.4	11	3	AAB14106	Aab14106 HLA DR B3
16	4	36.4	11	4	AAG65147	Aag65147 p21 deriv
17	4	36.4	11	4	AAY71871	Aay71871 Peptide #
18	4	36.4	11	4	ABP14414	Abp14414 HIV A03 s
19	4	36.4	11	4	ABP12457	Abp12457 HIV A02 s
20	4	36.4	11	4	ABP18569	Abp18569 HIV B62 s
21	4	36.4	11	4	ABP14413	Abp14413 HIV A03 s
22	4	36.4	11	4	ABP12458	Abp12458 HIV A02 s
23	4	36.4	11	5	ABP54087	Abp54087 Transport
24	4	36.4	11	5	AAE28549	Aae28549 scFv anti
25	4	36.4	11	7	ADC19832	Adc19832 Fluoresce
26	4	36.4	11	7	ADD57092	Add57092 HLA bindi
27	4	36.4	11	7	ADD57552	Add57552 HLA bindi
28	4	36.4	11	7	ADD57091	Add57091 HLA bindi
29	4	36.4	11	7	ADD57090	Add57090 HLA bindi
30	4	36.4	11	7	ADD57553	Add57553 HLA bindi
31	4	36.4	11	7	ADE52795	Ade52795 Human apo
32	3	27.3	11	1	AAP50987	Aap50987 FTS-deriv
33	3	27.3	11	1	AAP50941	Aap50941 Hepatitis
34	3	27.3	11	1	AAP60994	Aap60994 Sequence
35	3	27.3	11	1	AAP82045	Aap82045 "Peptide
36	3	27.3	11	1	AAP80853	Aap80853 Sequence
37	3	27.3	11	1	AAP93053	Aap93053 HIV env p
38	3	27.3	11	1	AAP90643	Aap90643 Signal pe
39	3	27.3	11	2	AAR04436	Aar04436 Human imm
40	3	27.3	11	2	AAR05607	Aar05607 Peptide a
41	3	27.3	11	2	AAR14094	Aar14094 Pre-S(1-1
42	3	27.3	11	2	AAR26439	Aar26439 N-termina
43	3	27.3	11	2	AAR24850	Aar24850 Weight re
44	3	27.3	11	2	AAR28129	Aar28129 Cell-to-c
45	3	27.3	11	2	AAR28133	Aar28133 Cell-to-c
46	3	27.3	11	2	AAR28088	Aar28088 Cell-to-c
47	3	27.3	11	2	AAR28135	Aar28135 Cell-to-c
48	3	27.3	11	2	AAR28090	Aar28090 Cell-to-c
49	3	27.3	11	2	AAR28131	Aar28131 Cell-to-c
50	3	27.3	11	2	AAR27175	Aar27175 Sequence
51	3	27.3	11	2	AAR29235	Aar29235 Heterocon
52	3	27.3	11	2	AAR32113	Aar32113 Light cha
53	3	27.3	11	2	AAR32411	Aar32411 Sequence
54	3	27.3	11	2	AAR33224	Aar33224 HIV gp120
55	3	27.3	11	2	AAR32352	Aar32352 Human Fac
56	3	27.3	11	2	AAR46532	Aar46532 Myelin ba
57	3	27.3	11	2	AAR38680	Aar38680 Bradykini
58	3	27.3	11	2	AAR40877	Aar40877 SSP for f
59	3	27.3	11	2	AAR41632	Aar41632 SSP for f
60	3	27.3	11	2	AAR40880	Aar40880 SSP for f
61	3	27.3	11	2	AAR37602	Aar37602 hIL2R Ab
62	3	27.3	11	2	AAR42981	Aar42981 MHC class
63	3	27.3	11	2	AAR62885	Aar62885 Murine an
64	3	27.3	11	2	AAR67043	Aar67043 Granulocy
65	3	27.3	11	2	AAR66140	Aar66140 CD-4 anti
66	3	27.3	11	2	AAR65955	Aar65955 N-termina

67	3	27.3	11	2	AAR52526	Aar52526 3D6 light
68	3	27.3	11	2	AAR52523	Aar52523 Gloop-2 l
69	3	27.3	11	2	AAR52525	Aar52525 36-71 lig
70	3	27.3	11	2	AAR85774	Aar85774 L-CDR-1 o
71	3	27.3	11	2	AAR74946	Aar74946 L-CDR-1 o
72	3	27.3	11	2	AAR85157	Aar85157 Human ONS
73	3	27.3	11	2	AAW21496	Aaw21496 Hepatitis
74	3	27.3	11	2	AAW21470	Aaw21470 Collagena
75	3	27.3	11	2	AAW21329	Aaw21329 Glucagon
76	3	27.3	11	2	AAR85505	Aar85505 ScFv(FWP5
77	3	27.3	11	2	AAR85502	Aar85502 ScFv(FRP)
78	3	27.3	11	2	AAR71311	Aar71311 GPV throm
79	3	27.3	11	2	AAY07532	Aay07532 Laminin-d
80	3	27.3	11	2	AAY07531	Aay07531 Laminin-d
81	3	27.3	11	2	AAR99018	Aar99018 Anti-thyr
82	3	27.3	11	2	AAR99009	Aar99009 Anti-thyr
83	3	27.3	11	2	AAR99015	Aar99015 Anti-thyr
84	3	27.3	11	2	AAW06143	Aaw06143 Adenoviru
85	3	27.3	11	2	AAW06144	Aaw06144 Adenoviru
86	3	27.3	11	2	AAR96840	Aar96840 N.gonorrh
87	3	27.3	11	2	AAR97313	Aar97313 Humanised
88	3	27.3	11	2	AAR90427	Aar90427 Antibody
89	3	27.3	11	2	AAW27566	Aaw27566 Anti-TNF-
90	3	27.3	11	2	AAW24543	Aaw24543 CDR #1 of
91	3	27.3	11	2	AAW36595	Aaw36595 MAGE-2 pe
92	3	27.3	11	2	AAW13942	Aaw13942 CDR-1 fra
93	3	27.3	11	2	AAW13937	Aaw13937 CDR-1 fra
94	3	27.3	11	2	AAW13919	Aaw13919 Generic f
95	3	27.3	11	2	AAW13920	Aaw13920 Fragment
96	3	27.3	11	2	AAW19410	Aaw19410 Anti-fung
97	3	27.3	11	2	AAW19456	Aaw19456 Anti-fung
98	3	27.3	11	2	AAW15672	Aaw15672 Platelet
99	3	27.3	11	2	AAW29348	Aaw29348 Cyclic hu
100	3	27.3	11	2	AAW34642	Aaw34642 Control p

ALIGNMENTS

RESULT 1
AAY88543
ID AAY88543 standard; peptide; 11 AA.
XX
AC AAY88543;
XX
DT 07-AUG-2000 (first entry)
XX
DE NCAM Ig1 binding peptide #15.
XX
KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW treatment; prosthetic nerve guide; treatment; nervous system.
XX
OS Synthetic.
XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Example 4; Page 25; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASQAKRRKGPR 11
|||||||||||
Db 1 ASQAKRRKGPR 11

RESULT 2
ABG69343

ID ABG69343 standard; peptide; 11 AA.

XX

AC ABG69343;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #15.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
KW postischaemic damage; multiinfarct dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
KW Alzheimer's disease; Parkinson's disease;
KW Huntington's disease. atrophic muscle disorder; gonad degeneration;
KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
CC impaired myelination of nerve fibres, postischaemic damage, e.g.
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
CC degeneration associated with diabetes mellitus, neuro-muscular
CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
CC Huntington's disease. The medicament is for the treatment of diseases or
CC conditions of the muscles including conditions with impaired function of
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
CC disorders, and for the treatment of diseases of conditions of various
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
CC ABG69352 represent human NCAM peptides of the invention

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQAKRRKGPR 11
|||
Db 1 ASQAKRRKGPR 11

RESULT 3
AAP82563
ID AAP82563 standard; peptide; 11 AA.
XX
AC AAP82563;
XX
DT 17-DEC-2001 (revised)
DT 19-NOV-1990 (first entry)
XX
DE HTLV-III env peptide for use as AIDS vaccine.
XX
KW AIDS; HTLV-III; envelope protein.
XX
OS Synthetic.
XX
PN USN6874913-N.
XX
PD 10-MAY-1988.
XX
PF 03-FEB-1986; 86US-00824913.
XX
PR 03-FEB-1986; 86US-00824913.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Heimer EP, Reddy PE, Gallo RC, Wongstaal F
XX

DR WPI; 1987-222902/32.
XX
PT New HTLV-III envelope peptide(s) - used for detecting presence of AIDS
PT antibodies, as vaccines and for producing antibodies.
XX
PS Disclosure; Page ?; 29pp; English.
XX
CC This peptide can have either (a) one or more amino acids from the N-
CC terminal residues 512-650 of HTLV-III envelope protein, or (b) one or
CC more amino acids from the C-terminal residues 460-499 of HTLV-III
CC envelope protein, attached to its C- or N- termini respectively. It is
CC useful for making immunogens to induce antibodies or to be used as
CC vaccines against AIDS. It can also be used to detect antibodies in blood.
CC (Note: Revised entry submitted to correct the patent number format of US
CC Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
||||
Db 2 AKRR 5

RESULT 4
AAR37408
ID AAR37408 standard; peptide; 11 AA.
XX
AC AAR37408;
XX
DT 25-MAR-2003 (revised)
DT 15-SEP-1993 (first entry)
XX
DE Factor X-derived peptide.
XX
KW Mac-1; macrophage-monocyte adhesive receptor; procoagulant; inflammation;
KW thrombosis; atherosclerosis; septic shock;
KW disseminated vascular coagulation; delayed hypersensitivity; haemostasis;
KW angiogenesis; leucocyte recruitment; adhesion.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "added amino terminal glycine residue"
FT .Misc-difference 11
FT /note= "added carboxy terminal glycine"
XX
PN WO9309803-A1.
XX
PD 27-MAY-1993.
XX

PF 20-NOV-1992; 92WO-US010068.
XX
PR 22-NOV-1991; 91US-00798221.
XX
PA (SCHA/) SCHAFFER S C.
PA (SCRI) SCRIPPS RES INST.
XX
PI Altieri DC, Edgington TS;
XX
DR WPI; 1993-182243/22.
XX
PT Factor X-derived polypeptide(s) inhibit binding of factor X to Mac-1 -
PT useful for treating thrombosis, atherosclerosis, disseminated
PT intravascular coagulation, septic shock etc.
XX
PS Disclosure; Page 106; 122pp; English.
XX
CC The sequence shown represents a fragment of the amino acid sequence of
CC human Factor X corresp. to a Mac-1 (macrophage-monocyte adhesive
CC receptor) recognition site. The fragment may be used to inhibit Factor Xa
CC monocyte procoagulant activity, specifically inflammation. The same
CC effect may be achieved with antibodies raised to the fragment. Typical
CC applications include treatment of patients at risk of thrombosis or
CC atherosclerosis before surgery, disseminated intra- vascular coagulation,
CC septic shock, inflammation caused by infection (esp. by herpes simplex)
CC or autoimmune diseases, delayed hyper- sensitivity, etc. The fragment
CC also inhibits leucocyte/endothelial cell interaction and thus regulates
CC responses such as leucocyte recruitment, adhesion and extravasation,
CC haematopoiesis, antigen presentation, angiogenesis, syncytial formation
CC and haemostasis. See also AAR37402-20. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
 ||||
Db 4 QAKR 7

RESULT 5
AAY04449
ID AAY04449 standard; peptide; 11 AA.
XX
AC AAY04449;
XX
DT 30-JUN-1999 (first entry)
XX
DE Myelin basic protein N-terminal peptide MBP Acl-11(4A).
XX
KW Myelin basic protein; MBP; antigenic; ovalbumin; copolymer; GVHD;
KW graft versus host disease; bone marrow transplantation.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "acetylated"
XX
PN WO9632119-A1.
XX
PD 17-OCT-1996.
XX
PF 15-APR-1996; 96WO-US005215.
XX
PR 14-APR-1995; 95US-00421412.
PR 06-OCT-1995; 95US-00540388.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Aharoni R, Arnon R, Chao NJ, Schlegel PG, Sela M, Teitelbaum D;
XX
DR WPI; 1996-476835/47.
XX
PT New synthetic peptide polymer designated GLAT copolymer - contg. Glu,
PT Lys, Ala and Tyr residues, used for preventing and treating graft-versus-
PT host disease.
XX
PS Example; Page 12; 43pp; English.
XX
CC The present invention describes a new synthetic random copolymer
CC (designated GLAT copolymer), which has an average molecular weight of
CC 4,000 - 12,000 and consists of Glu, Lys, Ala and Tyr residues in a
CC relative molar ratio of 1.4 - 2.1 parts of Glu to 3.2 - 5.0 parts of Lys
CC to 4.0 - 6.6 parts of Ala to 1.0 part of Tyr. The GLAT copolymer has the
CC ability to bind to multiple MHC class II molecules and inhibits antigen
CC presentation. It can be used for preventing and treating graft-versus-
CC host disease (GVHD) in patients, particularly in the course of bone
CC marrow or organ transplantation. The present sequence represents a
CC peptide used in the exemplification of the present invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
||||
Db 1 ASQA 4

RESULT 6
AAR93572
ID AAR93572 standard; peptide; 11 AA.
XX
AC AAR93572;
XX
DT 08-OCT-1996 (first entry)
XX

DE Dopamine receptor isoform D3 peptide analogue (aa: 22-32).
XX
KW Dopamine; identification; neurotransmitter; diagnosis; analogue;
KW isoform-specific antibody; receptor; distinguish; identification;
KW Parkinson's disease; Alzheimer's disease; neurological.
XX
OS Synthetic.
XX
PN WO9606856-A1.
XX
PD 07-MAR-1996.
XX
PF 30-AUG-1995; 95WO-US011127.
XX
PR 31-AUG-1994; 94US-00298600.
XX
PA (WEBB/) WEBBER R.
XX
PI Webber R;
XX
DR WPI; 1996-160304/16.
XX
PT Peptide analogues of different dopamine receptor isoform(s) - also
PT antibodies raised against them, useful in drug development and diagnosis,
PT e.g. of Parkinson's disease.
XX
PS Claim 1; Fig 3a; 56pp; English.
XX
CC AAR93572-R93575 are peptide analogues of the dopamine receptor isoform
CC D3. The analogues correspond to regions that are variable between the
CC five different isoforms, D1, D2, D3, D4 and D5 and as such are specific
CC for the particular isoform. The peptides or antibodies raised against
CC them are useful in developing drugs for the treatment of and diagnosis of
CC disorders related to the dopamine receptor e.g. Parkinson's disease and
CC Alzheimer's disease
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
|||
Db 2 ASQA 5

RESULT 7
AAW69570
ID AAW69570 standard; peptide; 11 AA.
XX
AC AAW69570;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1998 (first entry)
XX
DE Factor X peptide I.

XX
KW Factor X; filamentous haemagglutinin; FHA; endothelial cell;
KW integrin receptor; blood-brain barrier; antiinflammatory; inflammation;
KW meningitis; therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5792457-A.
XX
PD 11-AUG-1998.
XX
PF 06-JUN-1995; 95US-00465929.
XX
PR 03-MAY-1991; 91US-00695613.
PR 04-MAY-1992; 92WO-US003725.
PR 23-MAY-1994; 94US-00247572.
PR 30-NOV-1994; 94US-00348353.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Masure HR, Tuomanen E;
XX
DR WPI; 1998-456074/39.
XX
PT Increasing blood-brain barrier permeability - with antibody to
PT filamentous haemagglutinin RGD regions.
XX
PS Example 9; Col 32; 64pp; English.
XX
CC This peptide corresponds to amino acid residues 238-246 of Factor X.
CC Sequence similarity has been found between amino acid residues 238-246,
CC 366-374 and 422-430 (see AAW69568-70) of Factor X and amino acid residues
CC 1979-1984, 2063-2068, 32-36 and 2528-2533 (see AAW69571-74) of Bordetella
CC pertussis filamentous haemagglutinin (FHA). Inhibition of leukocyte-
CC endothelial cell interactions by FHA peptides which interact with
CC CD11b/CD18 in the same manner as Factor X was demonstrated. The FHA
CC peptides inhibit Factor Xa procoagulant activity on monocytes, and reduce
CC inflammation in an experimental meningitis model. Protection against
CC blood brain barrier permeability was also afforded by the FHA peptides.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
 ||||
Db 4 QAKR 7

RESULT 8
AAW39791
ID AAW39791 standard; protein; 11 AA.
XX

AC AAW39791;
XX
DT 11-JUN-1998 (first entry)
XX
DE Tobacco PABFa repeated AT hook.
XX
KW Palindromic element binding factor; PABF; tobacco; cis-acting element;
KW transcription enhancer; heterologous promoter; AATT repeat element;
KW transcription factor; AT hook.
XX
OS Nicotiana tabacum.
XX
PN WO9749727-A1.
XX
PD 31-DEC-1997.
XX
PF 27-JUN-1997; 97WO-US011156.
XX
PR 27-JUN-1996; 96US-00669721.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Lamb CJ, Doerner P, Laible G;
XX
DR WPI; 1998-077110/07.
XX
PT New isolated enhancer and transcription factor - used for increasing the
PT recombinant expression of proteins, particularly in plants, e.g. for
PT increasing production or providing pest resistance.
XX
PS Disclosure; Fig 7B; 65pp; English.
XX
CC AAW39790-W39796 are AT hook motifs used in the characterisation of a
CC novel tobacco palindromic element binding factor, (PABF). This PABF binds
CC to the sequence (AATT)_n where n at least 2. The (AATT)_n sequence has cis-
CC acting, non-specific enhancer activity. It can be linked to a
CC heterologous promoter operably linked with a gene to increase expression
CC of the gene in a cell, particularly in plants. It can provide for
CC increased expression of proteins such as nutritionally important
CC proteins, growth promoting factors, proteins for early flowering in
CC plants, proteins giving protection to the plant under certain
CC environmental conditions, e.g. proteins conferring resistance to metals
CC or other toxic substances, such as herbicides or pesticides, stress-
CC related proteins which confer tolerance to temperature extremes, proteins
CC conferring resistance to fungi, bacteria, viruses, insects and nematodes,
CC proteins of specific commercial value, e.g. enzymes involved in metabolic
CC pathways, such as EPSP synthase. The PABF polypeptides act as
CC transcription factor and bind to the (AATT) repeat element to further
CC boost the activity of the enhancer
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db ||||
 2 AKRR 5

RESULT 9

AAY43551

ID AAY43551 standard; peptide; 11 AA.

XX

AC AAY43551;

XX

DT 26-JAN-2000 (first entry)

XX

DE Peptide derived from human coagulation Factor X I.

XX

KW Filamentous hemagglutinin; FHA; Factor X; leukocyte;
KW blood vessel endothelial cell; migration; inflamed tissue;
KW non-fimbrial surface associated protein; *Bordetella pertussis*; C3bi;
KW RGD tripeptide; integrin receptor; inflammation; antibiotic therapy;
KW infection; meningitis; septic arthritis; endophthalmitis;
KW autoimmune disease.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN US5968512-A.

XX

PD 19-OCT-1999.

XX

PF 06-JUN-1995; 95US-00465965.

XX

PR 03-MAY-1991; 91US-00695613.

PR 04-MAY-1992; 92WO-US003725.

PR 23-MAY-1994; 94US-00247572.

PR 30-NOV-1994; 94US-00348353.

XX

PA (UYRQ) UNIV ROCKEFELLER.

XX

PI Masure HR, Tuomanen E;

XX

DR WPI; 1999-600812/51.

XX

PT Peptides inhibiting the influx of leukocytes into inflamed tissue, useful
PT for dampening inflammation during treatment with antibiotics.

XX

PS Claim 1; Col 75; 81pp; English.

XX

CC AAY43549-66 represent filamentous hemagglutinin (FHA) and Factor X
CC peptides which interact with leukocytes or with blood vessel endothelial
CC cells, thereby inhibiting the migration of leukocytes from the blood
CC stream into inflamed tissue. FHA is a non-fimbrial surface associated
CC protein secreted by *Bordetella pertussis*. As there are four regions in
CC FHA with sequence similarity to three regions in Factor X, some
CC antibodies to these four regions cross-react with Factor X, and vice
CC versa. The FHA peptides of the invention are derived from these regions.
CC FHA peptides competitively inhibit binding of Factor X and C3bi to
CC leukocytes. Specifically, the peptides inhibit the reaction between the
CC RGD tripeptide of FHA and the integrin receptors of endothelial cells.

CC The FHA peptides (and antibodies to them) dampen inflammation during the course of therapy with antibiotics and are therefore useful in the treatment of infections e.g. meningitis, septic arthritis, and endophthalmitis, and inflammation arising from autoimmune disease
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
|||
Db 4 QAKR 7

RESULT 10

AAY23947

ID AAY23947 standard; peptide; 11 AA.

XX

AC AAY23947;

XX

DT 20-MAR-2003 (revised)

DT 22-SEP-1999 (first entry)

XX

DE Peptide which blocks Factor X binding to leukocytes.

XX

KW Adhesion; leukocyte; endothelial cell; bacteria; *Bordetella pertussis*; ciliated respiratory epithelial cell; filamentous haemagglutinin; FHA; RGD region; cerebral endothelial cell; inflammation; antibiotic therapy; infection; meningitis; septic arthritis; endophthalmitis.

XX

OS Synthetic.

XX

PN US5932217-A.

XX

PD 03-AUG-1999.

XX

PF 30-NOV-1994; 94US-00348353.

XX

PR 03-MAY-1991; 91US-00695613.

PR 04-MAY-1992; 92WO-US003725.

PR 23-MAY-1994; 94US-00247572.

PR 14-JUL-1994; 94US-00140136.

XX

PA (UYRQ) UNIV ROCKEFELLER.

XX

PI Masure HR, Tuomanen E;

XX

DR WPI; 1999-443571/37.

XX

PT Peptides inhibiting the adhesion between leukocytes and endothelial cells, useful for treating inflammation.

XX

PS Example 9; Col 32; 82pp; English.

XX

CC The specification describes peptides which inhibit adhesion between

CC leukocytes and endothelial cells, and peptides which inhibit adhesion
CC between bacteria (*Bordetella pertussis*) and ciliated respiratory
CC epithelial cells. The specification also describes an immunogenic
CC composition comprising a polypeptide portion of *Bordetella pertussis*
CC filamentous haemagglutinin (FHA) containing no RGD region or containing
CC an amino acid sequence altered in the RGD region, where the polypeptide
CC portion elicits antibodies which do not cross-react with cerebral
CC endothelial cells. The peptides and methods are useful for reducing
CC inflammation during the course of antibiotic therapy of infectious
CC diseases such as meningitis, septic arthritis, and endophthalmitis. The
CC present sequence represents a peptide of the invention. (Updated on 20-
CC MAR-2003 to correct PR field.)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
 |||||
Db 4 QAKR 7

RESULT 11

AAY51590

ID AAY51590 standard; peptide; 11 AA.

XX

AC AAY51590;

XX

DT 12-SEP-2003 (revised)

DT 25-MAY-2000 (first entry)

XX

DE HIV-1 derived GP120 peptide fragment #2.

XX

KW Plastic carrier surface; detection; gp120.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200005584-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-NL000470.

XX

PR 21-JUL-1998; 98NL-01009703.

XX

PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOEK.

XX

PI Puijk WC;

XX

DR WPI; 2000-182757/16.

XX

PT Ultra flat plastic carrier surfaces by molding on to smooth non-adhesive
PT surfaces, e.g. mica or glass, and release, can carry active groups for
PT coupling to analytes, also form submicrotiter size wells suitable for
PT microprinting techniques.

XX
PS Disclosure; Fig 9; 47pp; English.
XX
CC This invention describes a novel method for the manufacture of an ultra flat plastic carrier surface, by laying on to a very smooth auxiliary surface, treating the plastic so that the surface roughness of the side facing the auxiliary is reduced, and removal; coupling of chemical and biochemical analytes for examination through active groups on the plastic surface; surface of plastic suitable for microjet printing techniques. Examples of applications of the surface include investigations of biological materials; peptides, proteins, saccharides, cells, viruses, antigens, and information carrying polymers, i.e. DNA or RNA, or their fragments, all optionally attached via linkers. Detection and determination of materials of interest can be carried out as in standard practice, e.g., ELISA, fluorescence, color, or radiation, except that very small amounts may be assayed or investigated. Conveniently, the surface can be as a matrix of microwells for these purposes; these can be molded into the surface by having hemispheres on the forming surface. The plastic surface is so smooth that it can bind very small amounts of materials of interest, which can be detected perfectly, even when close together on the surface by microscopy and/or photography, e.g., a confocal scanner, without interference from humps and hollows causing bad focussing. AAY51589-Y51596 represent peptide fragments derived from the human immunodeficiency virus type 1 gp120 protein which are used to illustrate the method of the invention. (Updated on 12-SEP-2003 to standardise OS field)
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
||||
Db 2 AKRR 5

RESULT 12

AAY67514

ID AAY67514 standard; peptide; 11 AA.

XX

AC AAY67514;

XX

DT 30-MAY-2000 (first entry)

XX

DE Factor X-like region comprising peptide fragment from FHA.

XX

KW FHA; blood-brain barrier; filamentous hemagglutinin; endothelial cell;
KW complement C3bi; factor X; integrin receptor CR3; leukocyte migration;
KW bacterial adhesion; brain cancer; acquired immune deficiency syndrome;
KW Parkinson's disease; Alzheimer's disease; antibacterial; anti-epileptic;
KW anti-inflammatory; anticancer; antiviral; antineurodegeneration.

XX

OS Bordetella pertussis.

XX

PN US6015560-A.

XX
PD 18-JAN-2000.
XX
PF 06-JUN-1995; 95US-00465966.
XX
PR 03-MAY-1991; 91US-00695613.
PR 04-MAY-1992; 92WO-US003725.
PR 23-MAY-1994; 94US-00247572.
PR 30-NOV-1994; 94US-00348353.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Masure HR, Tuomanen E;
XX
DR WPI; 2000-181133/16.
XX
PT Compositions containing antibody to filamentous hemagglutinin, used e.g.
PT to increase permeability of the blood-brain barrier and to inhibit
PT inflammation or bacterial adhesion.
XX
PS Disclosure; Col 8; 82pp; English.
XX
CC The invention provides a novel pharmaceutical composition for increasing
CC the permeability of the blood-brain barrier to a molecule (I). The
CC composition comprises (I) and an antibody to FHA (filamentous
CC hemagglutinin) which binds to endothelial cells in brain blood vessels,
CC increasing permeability. FHA contains polypeptide regions with binding
CC properties similar to those of complement C3bi, factor X and integrin
CC receptor CR3, and some anti-FHA antibodies are competitive inhibitors of
CC these materials, i.e. they reduce leukocyte migration or bacterial
CC adhesion. The compositions are used to improve delivery of (I) to the
CC brain, e.g. where (I) is used to treat brain cancer, acquired immune
CC deficiency syndrome, epilepsy, Parkinson's or Alzheimer's diseases or
CC other neurological diseases. Other antibodies directed against particular
CC regions of FHA are used to treat inflammation (caused by microbial
CC infection or auto-immune disease), also to prevent adhesion of *Bordetella*
CC pertussis to respiratory endothelial cells. Sequences AAY67512-515
CC represent FHA peptides having factor X-like regions
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
 |||||
Db 4 QAKR 7

RESULT 13
AAB14107
ID AAB14107 standard; peptide; 11 AA.
XX
AC AAB14107;
XX
DT 02-FEB-2001 (first entry)

XX
DE HLA DR B3.0201 peptide #6.
XX
KW gp 120; vaccine; AIDS; C5 region; immunotherapy; HLA DR beta chain; HIV.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 8..11
FT /note= "RRVV sequence is also found in gp120 peptide"
XX
PN WO200035480-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-GB004262.
XX
PR 15-DEC-1998; 98GB-00027603.
XX
PA (RETR-) RETROSCREEN LTD.
XX
PI Habeshaw JA, Hounsell E;
XX
DR WPI; 2000-442274/38.
XX
PT Vaccine comprising human immunodeficiency virus (HIV)-1 gp120 C5 peptide
PT core fragments, useful for vaccinating against HIV-1 induced acquired
PT immunodeficiency syndrome (AIDS).
XX
PS Disclosure; Page 28; 38pp; English.
XX
CC The present sequence is a HLA DR B3.0201 peptide. This sequence has a HIV
CC gp120 peptide-like binding motif. This sequence was used in a sequence
CC homology comparison with other HLA DR beta chain allele peptide fragments
CC (see AAB14096-B14106). The present invention relates to peptide fragments
CC from the C5 region of HIV-1 gp120 (see AAB13791-B13796). The HIV-1
CC peptides of the present invention may be used as a component of an
CC immunological composition which can be used for immunising or tolerising
CC an individual against AIDS
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 6 AKRR 9

RESULT 14
AAB14105
ID AAB14105 standard; peptide; 11 AA.
XX
AC AAB14105;
XX

DT 02-FEB-2001 (first entry)
XX
DE HLA DR B3.0201 peptide #4.
XX
KW gp 120; vaccine; AIDS; C5 region; immunotherapy; HLA DR beta chain; HIV.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 4..7
FT /note= "RRVV sequence is also found in gp120 peptide"
XX
PN WO200035480-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-GB004262.
XX
PR 15-DEC-1998; 98GB-00027603.
XX
PA (RETR-) RETROSCREEN LTD.
XX
PI Habeshaw JA, Hounsell E;
XX
DR WPI; 2000-442274/38.
XX
PT Vaccine comprising human immunodeficiency virus (HIV)-1 gp120 C5 peptide
PT core fragments, useful for vaccinating against HIV-1 induced acquired
PT immunodeficiency syndrome (AIDS).
XX
PS Disclosure; Page 28; 38pp; English.
XX
CC The present sequence is a HLA DR B3.0201 peptide. This sequence has a HIV
CC gp120 peptide-like binding motif. This sequence was used in a sequence
CC homology comparison with other HLA DR beta chain allele peptide fragments
CC (see AAB14096-B14104 and AAB14106-B14107). The present invention relates
CC to peptide fragments from the C5 region of HIV-1 gp120 (see AAB13791-
CC B13796). The HIV-1 peptides of the present invention may be used as a
CC component of an immunological composition which can be used for
CC immunising or tolerising an individual against AIDS
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
Db 2 AKRR 5

RESULT 15
AAB14106
ID AAB14106 standard; peptide; 11 AA.
XX
AC AAB14106;

XX
DT 02-FEB-2001 (first entry)
XX
DE HLA DR B3.0201 peptide #5.
XX
KW gp 120; vaccine; AIDS; C5 region; immunotherapy; HLA DR beta chain; HIV.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 7. .10
FT /note= "RRVV sequence is also found in gp120 peptide"
XX
PN WO200035480-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-GB004262.
XX
PR 15-DEC-1998; 98GB-00027603.
XX
PA (RETR-) RETROSCREEN LTD.
XX
PI Habeshaw JA, Hounsell E;
XX
DR WPI; 2000-442274/38.
XX
PT Vaccine comprising human immunodeficiency virus (HIV)-1 gp120 C5 peptide
PT core fragments, useful for vaccinating against HIV-1 induced acquired
PT immunodeficiency syndrome (AIDS).
XX
PS Disclosure; Page 28; 38pp; English.
XX
CC The present sequence is a HLA DR B3.0201 peptide. This sequence has a HIV
CC gp120 peptide-like binding motif. This sequence was used in a sequence
CC homology comparison with other HLA DR beta chain allele peptide fragments
CC (see AAB14096-B14105 and AAB14107). The present invention relates to
CC peptide fragments from the C5 region of HIV-1 gp120 (see AAB13791-
CC B13796). The HIV-1 peptides of the present invention may be used as a
CC component of an immunological composition which can be used for
CC immunising or tolerising an individual against AIDS
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 5 AKRR 8

RESULT 16
AAG65147
ID AAG65147 standard; peptide; 11 AA.
XX

AC AAG65147;
XX
DT 21-NOV-2001 (first entry)
XX
DE p21 derived cyclin A binding peptide #1.
XX
KW Human; p21WAF1; cyclin dependent protein kinase; CDK2; cyclin A;
KW inhibitor; proliferative disorder; cancer; leukaemia; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Hydrogenated N-terminus"
FT Misc-difference 5
FT /note= "Wild-type Ser substituted by Ala"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200140142-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-GB004550.
XX
PR 30-NOV-1999; 99GB-00028323.
XX
PA (CYCL-) CYCLACEL LTD.
XX
PI Zheleva DI, Fischer PM, McInnes C, Andrews MJI, Chan WC;
PI Atkinson GE;
XX
DR WPI; 2001-488493/53.
XX
PT New p21 derived peptides and their variants, particularly useful as
PT selective inhibitors of CDK2/cyclin interaction for treating
PT proliferative disorders e.g. cancers and leukemias, and in assays for
PT identifying CDK/cyclin inhibitors.
XX
PS Example 10; Page 51; 102pp; English.
XX
CC The invention relates to peptide and their variants derived from p21WAF1,
CC which are inhibitors of CDK2 activity by binding to G1 and S phase
CC specific cyclins which activate CDK2; selective inhibitors of CDK2/cyclin
CC complexes, particularly CDK2/cyclin A or E complexes. The variants of the
CC peptide may have further amino acids at either end or have up to 7 amino
CC acids deleted, provided the motif XLXF is retained. The peptides are
CC specific regions of p21WAF1 that bind to G1 and S phase specific cyclins,
CC preferably cyclins which activate CDK2. One of the peptides corresponds
CC to p21(149-159). The peptides are used for treating proliferative
CC disorders, e.g. cancers and leukemias. The peptides are also for
CC identifying substances which interfere with protein-protein interactions
CC involving cyclins (i.e. cyclin A, E or D), especially CDK/cyclin
CC interactions, and which are capable of inhibiting CDK2 and/or CDK4
CC activity. P21 peptides other than p21(149-159) competitively inhibit the

CC binding of peptide p21(149-159) to cyclin and may be used to identify
CC substances that bind to, or inhibit peptide- cyclin interactions.
CC Substances for screening in the assays include antibody products specific
CC for p21 or cyclin binding regions, combinatorial libraries and single
CC compound collections. The present sequence is a peptide derived from the
CC C-terminus of p21 and used in a Cyclin A binding experiment

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7

||||

Db 5 AKRR 8

RESULT 17

AAY71871

ID AAY71871 standard; peptide; 11 AA.

XX

AC AAY71871;

XX

DT 26-MAR-2001 (first entry)

XX

DE Peptide #3, internal sequence of SmaA protein.

XX

KW Fimbrial-associated adhesion; SmaA; antibacterial;
KW amylase-binding protein; dental cary; vaccine; oral cavity.

XX

OS Streptococcus mutans.

XX

PN WO200066616-A1.

XX

PD 09-NOV-2000.

XX

PF 03-MAY-2000; 2000WO-US011992.

XX

PR 03-MAY-1999; 99US-0132312P.

XX

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX

PI Gregory RL;

XX

DR WPI; 2001-024770/03.

XX

PT Controlling dental caries in the oral cavity of a host comprises
PT administering purified SmaA protein or an amylase-binding polypeptide
PT fragment to the oral cavity.

XX

PS Disclosure; Page 14; 67pp; English.

XX

CC The present sequence is an internal peptide of Streptococcus mutans
CC fimbrial-associated adhesion protein, SmaA. The SmaA protein has
CC antibacterial activity and acts as an inhibitor of dental caries. The
CC SmaA protein is useful for controlling dental caries in the oral cavity.

CC An oral composition containing SmaA protein or an amylase-binding protein
CC blocks attachment of caries-causing bacteria *S. mutans* to the salivary
CC pellicle. Recombinant SmaA protein is used in the implementation of
CC vaccines against dental caries

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQAK 5
|||
Db 3 SQAK 6

RESULT 18

ABP14414

ID ABP14414 standard; peptide; 11 AA.

XX

AC ABP14414;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 super motif env peptide #154.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 164; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7
||||
Db 2 AKRR 5

RESULT 19
ABP12457
ID ABP12457 standard; peptide; 11 AA.
XX
AC ABP12457;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #514.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 124; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 7 AKRR 10

RESULT 20
ABP18569
ID ABP18569 standard; peptide; 11 AA.
XX
AC ABP18569;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV B62 super motif env peptide #144.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 249; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 7 AKRR 10

RESULT 21
ABP14413
ID ABP14413 standard; peptide; 11 AA.
XX
AC ABP14413;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 super motif env peptide #153.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 164; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 4 AKRR 7

RESULT 22

ABP12458

ID ABP12458 standard; peptide; 11 AA.

XX

AC ABP12458;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif env peptide #515.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 124; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 6 AKRR 9

RESULT 23

ABP54087

ID ABP54087 standard; peptide; 11 AA.

XX

AC ABP54087;

XX

DT 15-JAN-2003 (first entry)

XX

DE Transport moiety cellular uptake peptide #11.

XX

KW Transporter; Spaced arginine moiety; vasotropin; neuroleptic; analgesic;
KW antiparkinsonian; biologically active compound; biological membrane;
KW epithelial tissue; endothelial tissue; ischaemia; neurotransmitter;
KW schizophrenia; Parkinson's disease; pain; transport moiety.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1
FT /label= Acp
FT /note= "epsilon-aminocaproic acid (aca); N-terminally
FT modified with fluorescein (Fl)"
FT Modified-site 11
FT /note= "C-terminally modified with CONH2"

XX

PN WO200265986-A2.

XX

PD 29-AUG-2002.

XX
PF 14-FEB-2002; 2002WO-US004491.
XX
PR 16-FEB-2001; 2001US-00269627.
XX
PA (CELL-) CELLGATE INC.
XX
PI Wender PA, Rothbard JB, Wright L, Kreider EL, Vandeusen CL;
XX
DR WPI; 2002-740700/80.
XX
PT Composition, useful for increasing the transport of a biologically active compound across a biological membrane, comprises a biologically active compound and a transport moiety.
XX
PS Example 1; Page 24; 58pp; English.
XX
CC The present invention describes a composition (C) comprising a biologically active compound (A) and a transport moiety (B) of formula: (ZYZ)_nZ (I), (ZY)_nZ (II), (ZYY)_nZ (III) or (ZYYY)_nZ (IV), where Z = L-arginine or D-arginine; Y = amino acid (not comprising amidino or guanidino moiety); and n = 2-10. Also described is a method for increasing the transport of a biologically active compound across a biological membrane involving administering (C). (C) has vasotropic, neuroleptic, antiparkinsonian and analgesic activities. (C) is used for increasing the transport of a biologically active compound across a biological membrane and across and into animal epithelial or endothelial tissues. (C) can be used for treating ischaemia and delivering neurotransmitters and other agents for treating schizophrenia, Parkinson's disease and pain. The transport of the biologically active compound across the biological membrane is increased relative to the transport of the biologically active compound in the absence of the transport moiety. The present sequence represents a transport moiety cellular uptake peptide, which is used in an example from the present invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRRK 8
|||
Db 3 KRRK 6

RESULT 24
AAE28549
ID AAE28549 standard; peptide; 11 AA.
XX
AC AAE28549;
XX
DT 27-DEC-2002 (first entry)
XX
DE scFv antibody light chain CDR2 from S18 clone.
XX

KW Human; sugar-nucleic acid interaction; single chain human antibody; scFv;
KW L-peptide binder; D-nucleic acid binder; sugar-protein interaction; CDR2;
KW complementarity determining region 2.
XX
OS Homo sapiens.
XX
PN WO200267860-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005193.
XX
PR 22-FEB-2001; 2001US-0271377P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Wong C;
XX
DR WPI; 2002-691633/74.
XX
PT Selecting L-peptide or D-nucleic acid binders that binds to enantiomers
PT of naturally occurring carbohydrate, comprises providing enantiomers of
PT naturally occurring carbohydrate, and screening library against
PT enantiomers.
XX
PS Disclosure; Fig 6B; 46pp; English.
XX
CC The present invention relates to a novel method of selecting L-peptide or
CC D-nucleic acid binders that bind to enantiomers of naturally occurring
CC sugar or carbohydrate. The method involves providing enantiomers of
CC naturally occurring sugar or carbohydrate employable for screening the
CC library and then screening the library against the enantiomers for
CC identifying a L-peptide binder or D-nucleic acid binder having binding
CC activity with respect to enantiomers. The method is useful for selecting
CC L-peptide binder or D-nucleic acid binder that binds to enantiomer of
CC naturally occurring sugar or carbohydrate. It is useful for selecting L-
CC peptide binders and/or L-nucleic acid binders that are resistant to
CC enzymatic degradation due to their non-naturally occurring chirality, for
CC blocking or activating the biological function of the naturally occurring
CC sugar or carbohydrate to which they are targeted. The naturally occurring
CC sugars and carbohydrates include bacterial or viral cell surface sugars
CC or carbohydrates, heparin sulphates involved in viral entry, thrombosis
CC and angiogenesis. The method is useful for identifying D-peptides, for
CC studying sugar-protein and sugar-nucleic acid interaction and for
CC designing high-affinity and hydrolase resistant molecules as artificial
CC receptors capable of binding natural carbohydrates. The immobilised
CC enantiomers are useful for screening phage expressing a peptide library
CC on the coat proteins to identify specific clones that bind to an
CC immobilised enantiomer. The present sequence is single chain human
CC antibody (scFv) light chain complementarity determining region 2 (CDR2)
CC from S18 clone. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKGP 10
||||
Db 8 RKGP 11

RESULT 25

ADC19832

ID ADC19832 standard; peptide; 11 AA.

XX

AC ADC19832;

XX

DT 18-DEC-2003 (first entry)

XX

DE Fluorescently labelled spaced arginine transport peptide #12.

XX

KW Cellular membrane transport peptide; epithelial tissue;
KW endothelial tissue; drugs transport; stratum corneum; antibacterial;
KW antifungal; antiviral; antiproliferative; immunosuppressive; vitamin;
KW analgesic; hormone.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label

FT /note= "Xaa is fluorescently labelled epsilon-
FT aminocaprylic acid"

FT Modified-site 11

FT /label= OTHER

FT /note= "Arg is covalently bound to a CONH2 group"

XX

PN US2003032593-A1.

XX

PD 13-FEB-2003.

XX

PF 14-FEB-2002; 2002US-00078247.

XX

PR 16-FEB-2001; 2001US-0269627P.

XX

PA (CELL-) CELLGATE INC.

XX

PI Wender PA, Rothbard JB, Wright L, Kreider EL, Vandeusen CJ;

XX

DR WPI; 2003-786846/74.

XX

PT Composition used for increasing transport of biologically active compound
PT across biological membrane comprises biologically active compound and
PT transport group.

XX

PS Example 1; Page 9; 33pp; English.

XX

CC The invention relates to a composition comprising a biologically active
CC compound and a transport group. The transport group comprises a spaced
CC poly-Arginine based peptide of formula given in the specification. The
CC spaced poly-Arginine based peptide acts as a cellular membrane transport

CC signal and effects transport of the biologically active compound across
CC the membrane. The conjugate is also useful in therapeutic, prophylactic
CC and diagnostic applications. The composition improves the transport of
CC biologically active compounds across the biological membrane and into
CC animal epithelial or endothelial tissues. The arginine residue of the
CC conjugate provides an enhanced transport of drugs and are a part of the
CC polypeptide that provides suitable spacing between arginine residues. The
CC transport groups deliver an agent across the stratum corneum, which
CC previously had been a nearly impenetrable barrier to drug delivery. The
CC ability of the conjugate to obtain penetration of skin layers improves
CC the efficacy of compounds such as antibacterials, antifungals,
CC antivirals, antiproliferatives, immunosuppressives, vitamins, analgesics
CC and hormones. The present sequence is a Fluorescently labelled spaced
CC arginine transport peptide of the invention.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRRK 8
 ||||
Db 3 KRRK 6

RESULT 26

ADD57092

ID ADD57092 standard; peptide; 11 AA.

XX

AC ADD57092;

XX

DT 15-JAN-2004 (first entry)

XX

DE HLA binding epitope #312.

XX

KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.

XX

OS Unidentified.

XX

PN WO2003040165-A2.

XX

PD 15-MAY-2003.

XX

PF 18-OCT-2001; 2001WO-US051650.

XX

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S;

XX

DR WPI; 2003-441519/41.

XX

PT New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADD56781-
CC ADD65275 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRGKG 9
|||
Db 5 RRGKG 8

RESULT 27
ADD57552
ID ADD57552 standard; peptide; 11 AA.
XX
AC ADD57552;
XX
DT 15-JAN-2004 (first entry)
XX
DE HLA binding epitope #772.
XX
KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.
XX
OS Unidentified.
XX
PN WO2003040165-A2.
XX
PD 15-MAY-2003.
XX
PF 18-OCT-2001; 2001WO-US051650.
XX

PR 19-OCT-2000; 2000US-0242350P.
PR 20-APR-2001; 2001US-0285624P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2003-441519/41.
XX
PT New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADD56781-
CC ADD65275 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRKG 9
|||
Db 5 RRKG 8

RESULT 28
ADD57091
ID ADD57091 standard; peptide; 11 AA.
XX
AC ADD57091;
XX
DT 15-JAN-2004 (first entry)
XX
DE HLA binding epitope #311.
XX
KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.

XX
OS Unidentified.
XX
PN WO2003040165-A2.
XX
PD 15-MAY-2003.
XX
PF 18-OCT-2001; 2001WO-US051650.
XX
PR 19-OCT-2000; 2000US-0242350P.
PR 20-APR-2001; 2001US-0285624P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2003-441519/41.
XX
PT New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
CC The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADD56781-ADD65275 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRGKG 9
||||
Db 5 RRGKG 8

RESULT 29
ADD57090
ID ADD57090 standard; peptide; 11 AA.
XX

AC ADD57090;
XX
DT 15-JAN-2004 (first entry)
XX
DE HLA binding epitope #310.
XX
KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.
XX
OS Unidentified.
XX
PN WO2003040165-A2.
XX
PD 15-MAY-2003.
XX
PF 18-OCT-2001; 2001WO-US051650.
XX
PR 19-OCT-2000; 2000US-0242350P.
PR 20-APR-2001; 2001US-0285624P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2003-441519/41.
XX
PT New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADD56781-
CC ADD65275 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRKG 9
 ||||
Db 5 RRKG 8

RESULT 30

ADD57553

ID ADD57553 standard; peptide; 11 AA.

XX

AC ADD57553;

XX

DT 15-JAN-2004 (first entry)

XX

DE HLA binding epitope #773.

XX

KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KW viral disease; cancer.

XX

OS Unidentified.

XX

PN WO2003040165-A2.

XX

PD 15-MAY-2003.

XX

PF 18-OCT-2001; 2001WO-US051650.

XX

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S;

XX

DR WPI; 2003-441519/41.

XX

PT New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.

XX

PS Claim 1; Page 52-379; 382pp; English.

XX

CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies

CC and for evaluating efficacy of a vaccine. Sequences given in ADD56781-
CC ADD65275 represent epitopes of the invention as given in Tables 2-31.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRGKG 9
Db 5 RRGKG 8

RESULT 31

ADE52795

ID ADE52795 standard; peptide; 11 AA.

XX

AC ADE52795;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human apoptin NLS2 peptide.

XX

KW human; apoptin; NLS; nuclear localisation signal;

KW aberrant-specific apoptosis; cytostatic; immunosuppressive; gene therapy;

KW cell proliferation; cancer; autoimmune disease.

XX

OS Homo sapiens.

XX

PN WO2003089467-A1.

XX

PD 30-OCT-2003.

XX

PF 18-MAR-2003; 2003WO-NL000195.

XX

PR 19-APR-2002; 2002EP-00076597.

XX

PA (LEAD-) LEADD BV.

XX

PI Noteborn MHM, Danen-Van Oorschot AAM;

XX

DR WPI; 2003-845522/78.

XX

PT New fragment of Apoptin that induces aberrant-specific apoptosis, useful
PT in preparing a medicament for treating a disease associated with enhanced
PT cell proliferation or decreased cell death, e.g., cancer or autoimmune
PT disease.

XX

PS Disclosure; Page 23; 46pp; English.

XX

CC The invention relates to a novel isolated or recombinant fragment of
CC Apoptin that is capable of inducing aberrant-specific apoptosis. A
CC peptide of the invention has cytostatic, and immunosuppressive activity,
CC and may have a use in gene therapy. The fragment of Apoptin, nucleic
CC acid, vector, gene delivery vehicle or host cell is useful in preparing a
CC medicament for treating a disease where enhanced cell proliferation or

CC decreased cell death is observed, e.g., cancer or autoimmune disease. The
CC present sequence is used in the exemplification of the invention.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
||||
Db 5 AKRR 8

RESULT 32

AAP50987

ID AAP50987 standard; peptide; 11 AA.

XX

AC AAP50987;

XX

DT 25-MAR-2003 (revised)

DT 08-MAR-1992 (first entry)

XX

DE FTS-derived peptide.

XX

KW Serum thymus factor; FTS.

XX

OS Synthetic.

XX

PN JP60089499-A.

XX

PD 20-MAY-1985.

XX

PF 21-OCT-1983; 83JP-00196079.

XX

PR 21-OCT-1983; 83JP-00196079.

XX

PA (MITH) MITSUI PHARM INC.

XX

DR WPI; 1985-156917/26.

XX

PT New peptide for use in analysis - derived from lysine, tyrosine, glycine,
PT alanine, serine and asparagine units.

XX

PS Claim 1; Page 1; 12pp; Japanese.

XX

CC The peptide is derived from FTS (Pyr-Ala-Lys-Ser-Gln-Gly-Gly-Ser-Asn). It
CC has similar activity to FTS and can be easily labelled with radioactive
CC iodide for use in RIA. See also AAP50412 and AAP50413. (Updated on 25-MAR
CC -2003 to correct PR field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAK 5
 |||
Db 3 QAK 5

RESULT 33
AAP50941
ID AAP50941 standard; peptide; 11 AA.
XX
AC AAP50941;
XX
DT 25-MAR-2003 (revised)
DT 06-OCT-1991 (first entry)
XX
DE Hepatitis B virus (HBV) envelope protein pre-S gene peptide fragment.
XX
KW Immunogen; vaccine; antigen; epitope; diagnosis.
XX
OS Hepatitis B virus.
XX
PN EP154902-A.
XX
PD 18-SEP-1985.
XX
PF 28-FEB-1985; 85EP-00102250.
XX
PR 07-MAR-1984; 84US-00587090.
PR 05-FEB-1985; 85US-00698499.
PR 28-APR-1986; 86US-00856522.
XX
PA (CALY) CALIFORNIA INST OF TECHN.
PA (NYBL-) NEW YORK BLOOD CENTER INC.
XX
PI Neurath AR, Kent SBH;
XX
DR WPI; 1985-237979/39.
XX
PT Pre-s-gene coded hepatitis B immunogens - useful in vaccines for
PT protection and as diagnostics for detection of antigens and antigens.
XX
PS Claim 30; Page 101; 140pp; English.
XX
CC The peptides of the invention are immunogens which, esp. when linked to
CC carriers, may be used in vaccines for conferring protection against HBV,
CC and in the diagnosis of viral conditions in man and animals and in the
CC detection of the antigens and antibodies. More specifically, the chain of
CC AAs is between sequence posn. pre-S 120-174. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKG 9
 |||

Db 9 RKG 11

RESULT 34
AAP60994
ID AAP60994 standard; peptide; 11 AA.
XX
AC AAP60994;
XX
DT 08-AUG-1991 (first entry)
XX
DE Sequence of immunogenic fragment of apolipoprotein (APL) ApoA2.
XX
KW Apolipoprotein; immunoassay; antibody.
XX
OS Homo sapiens.
XX
PN WO8604144-A.
XX
PD 17-JUL-1986.
XX
PF 26-DEC-1985; 85WO-US002569.
XX
PR 31-DEC-1984; 84US-00688040.
XX
PA (ITGE-) INT GENETIC ENG INC.
XX
PI Fareed G, Sen A;
XX
DR WPI; 1986-196930/30.
XX
PT Peptide fragments of human apo:lipoprotein - used for producing type-specific antibodies for immunoassay.
XX
PS Claim 27; Page 39; 53pp; English.
XX
CC The peptides of the invention are conjugated with carrier proteins and
CC used to produce type-specific, non-cross-reactive antibodies by
CC immunisation. The antibodies may then be used in immunoassays to identify
CC and quantitate specific APIs. Peptide fragments without the C-terminal
CC Cys residue are also claimed
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAK 5
|||
Db 1 QAK 3

RESULT 35
AAP82045
ID AAP82045 standard; peptide; 11 AA.
XX

AC AAP82045;
XX
DT 19-OCT-1990 (first entry)
XX
DE "Peptide 3" consisting of residues 37-47 of amyloid A protein.
XX
KW Amyloid A protein; secondary amyloidosis; anti-amyloid A antibody.
XX
OS Synthetic.
XX
PN JP63044895-A.
XX
PD 25-FEB-1988.
XX
PF 13-AUG-1986; 86JP-00189810.
XX
PR 13-AUG-1986; 86JP-00189810.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
DR WPI; 1988-094820/14.
XX
PT Anti-amyloid-A protein monoclonal antibody - used esp. for detection of
PT sec. amyloidosis.
XX
PS Claim 2; Page 649; 6pp; Japanese.
XX
CC An antibody capable of recognising Amyloid A and this peptide but which
CC does not react with other specified peptides (see AAP82046-9) is useful
CC for detection of secondary amyloidosis
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 9 AKR 11

RESULT 36
AAP80853
ID AAP80853 standard; protein; 11 AA.
XX
AC AAP80853;
XX
DT 15-JAN-1991 (first entry)
XX
DE Sequence of N-terminal pre-porcine growth hormone encoded on plasmid
DE pKTGH.
XX
KW Transgenic animal; somatotrophin.
XX
OS Sus scrofa.
XX

PN WO8808026-A.
XX
PD 20-OCT-1988.
XX
PF 14-APR-1988; 88WO-AU000109.
XX
PR 14-APR-1987; 87AU-00001427.
PR 17-APR-1987; 88AU-00017004.
PR 10-NOV-1987; 87AU-00005326.
XX
PA (LUMI-) LUMINIS PTY LTD.
XX
PI Seamark RF, Wells JR;
XX
DR WPI; 1988-307564/43.
DR N-PSDB; AAN80881.
XX
PT Creating new breed(s) of animals - by introducing a gene sample of a
PT hormone homologous with the ovum into the male nucleus of a fertilised
PT ovum.
XX
PS Example; Fig 6; 35pp; English.
XX
CC A method for creating new breeds of animals comprises (a) obtaining a
CC recently fertilised ovum, (b) isolating a gene sample of a characterising
CC hormone homologous with the ovum, (c) introducing the gene sample into
CC the male nucleus of the ovum prior to fusion with the female nucleus to
CC form a single cell embryo and (d) subsequently implanting the ovum into a
CC suitably prep'd. female animal. Also claimed is a plasmid expression
CC vector comprising a plasmid cloning vector including a first cloned
CC sequence of DNA encoding a non-porcine promoter region and a second
CC cloned sequence encoding porcine growth hormone activity
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 4 GPR 6

RESULT 37
AAP93053
ID AAP93053 standard; peptide; 11 AA.
XX
AC AAP93053;
XX
DT 01-JUN-1994 (revised)
DT 11-JUN-1990 (first entry)
XX
DE HIV env protein analogue (j).
XX
KW HIV; human immunodeficiency virus; envelope protein; AIDS; vaccine;
KW antigen; epitope; antibody; infection.

XX
OS Synthetic.
XX
PN EP298633-A.
XX
PD 11-JAN-1989.
XX
PF 24-JUN-1988; 88EP-00305771.
XX
PR 24-JUN-1987; 87GB-00014802.
XX
PA (PROT-) PROTEUS BIOTECHN LT.
XX
PI Fishleigh RV, Robson B;
XX
DR WPI; 1989-009700/02.
XX
PT Synthetic polypeptide analogues of envelope protein of HIV - used as
PT vaccines, for producing antibodies and treating HIV infections.
XX
PS Claim 1 + 7-8; Page 7-8; 8pp; English.
XX
CC The polypeptide optionally has the second A, the L and the V replaced by
CC any residue, partic. the second A is replaced by E, the L by I and/or the
CC V by F. The antigenic polypeptide, either alone or linked to a carrier,
CC may be used as a vaccine against one or more strains of HIV; for
CC generation of antibodies, for study of the HIV virus and in diagnosis;
CC and for treatment of HIV infections by displacing the binding of the
CC virus or by disturbing the 3-D organisation
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 9 AKR 11

RESULT 38
AAP90643
ID AAP90643 standard; protein; 11 AA.
XX
AC AAP90643;
XX
DT 10-MAR-2003 (revised)
DT 09-AUG-1990 (first entry)
XX
DE Signal peptide NOS Synthetic.
XX
KW NOS; signal peptide; nucleolus.
XX
OS Unidentified.
XX
PN JP01096196-A.

XX
PD 14-APR-1989.
XX
PF 08-OCT-1987; 87JP-00252377.
XX
PR 08-OCT-1987; 87JP-00252377.
XX
PA (HATA/) HATANAKA S.
XX
DR WPI; 1989-155085/21.
XX
PT New peptide NOS having specific aminoacid sequence - used to localise
PT protein in nucleolus.
XX
PS Claim 1; Page 1; 12pp; Japanese.
XX
CC The peptide is useful for localising a protein in the nucleolus. DNA
CC encoding it is inserted downstream of promoter in a plasmid to give pNOS
CC Synthetic. DNA encoding an opt protein is also ligated into the vector,
CC and the pNOS introduced to a host (eg E.coli). Plasmid DNA is then
CC extracted from the cells and transfected into eukaryotic cells which have
CC a nucleolus. Protein localisation can be detected immunologically within
CC hours. See also AAP90642-4. (Updated on 10-MAR-2003 to add missing OS
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 4 KRR 6

RESULT 39
AAR04436
ID AAR04436 standard; protein; 11 AA.
XX
AC AAR04436;
XX
DT 25-MAR-2003 (revised)
DT 20-SEP-1990 (first entry)
XX
DE Human immunodeficiency virus peptide 339.
XX
KW HIV-RF; peptide 339; principal neutralising domain; antibodies;
KW prophylaxis; therapy; AIDS.
XX
OS Synthetic.
XX
PN WO9003984-A.
XX
PD 19-APR-1990.
XX
PF 03-OCT-1988; 88US-00252949.

XX
PR 03-OCT-1988; 88US-00252949.
PR 01-JUN-1989; 89US-00359543.
PR 19-SEP-1989; 89US-00407663.
XX
PA (REPK) REPLIGEN CORP.
XX
PI Rusche JR, Putney SD, Javaherian K, Farley J, Grimalia R;
PI Lynn DU, Petrobre J;
XX
DR WPI; 1990-147824/19.
XX
PT Principal neutralising domain of HIV variants - used for producing
PT peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy
PT therapy therapy of HIV infection.
XX
PS Claim 8 (39); Page 76; 108pp; English.
XX
CC Peptide 339 comprises segments of the Principal Neutralising Domain
CC (envelope protein) from isolate HIV-RF. The last Cys residue is added for
CC the purpose of crosslinking to carrier proteins. Cysteine residues can be
CC added so that residues at or near both ends form a disulfide bond,
CC thus giving the peptide a loop-like configuration, which is utilised to
CC enhance the immunogenic properties of the peptide. The peptide is capable
CC of eliciting, and/or binding with, neutralising antibodies. The
CC neutralising domain is bounded by cysteine residues which occur at
CC positions 296 and 331. Peptides can be used as immunogens or screening
CC reagents to generate or identify poly- or monoclonal Abs. See also
CC AAR04427-R04506 and AAQ04273-Q04279. (Updated on 25-MAR-2003 to correct
CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct PI field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 3 KGP 5

RESULT 40
AAR05607
ID AAR05607 standard; protein; 11 AA.
XX
AC AAR05607;
XX
DT 25-MAR-2003 (revised)
DT 26-OCT-1990 (first entry)
XX
DE Peptide antigenic for human papilloma virus.
XX
KW Human papilloma virus; HPV16.
XX
OS Synthetic.

XX
PN EP375555-A.
XX
PD 27-JUN-1990.
XX
PF 21-DEC-1989; 89EP-00403601.
XX
PR 23-DEC-1988; 88FR-00017097.
XX
PA (MEDG-) MEDGENIX GROUP SA.
PA (DMAR/) DE MARTYNOFF G.
XX
PI Demartynof G, Brasseur R, Zeicher M;
XX
DR WPI; 1990-195643/26.
XX
PT New papilloma virus peptide(s) - contg. antigenic determinants, for
PT diagnostic use.
XX
PS Claim 1; Page 11; 14pp; French.
XX
CC Peptides can be used to raise Abs, useful in immunoassay of HPV16
CC proteins. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 7 AKR 9

RESULT 41
AAR14094
ID AAR14094 standard; protein; 11 AA.
XX
AC AAR14094;
XX
DT 25-MAR-2003 (revised)
DT 04-DEC-1991 (first entry)
XX
DE Pre-S(1-11) immunogenic peptide based on HBV subtype adw2.
XX
KW hepatitis B virus; vaccine; liposome-peptide complex.
XX
OS Synthetic.
XX
PN EP448126-A.
XX
PD 25-SEP-1991.
XX
PF 28-FEB-1985; 91EP-00105948.
XX
PR 07-MAR-1984; 84US-00587090.

PR 05-FEB-1985; 85US-00698499.
XX
PA (NYBL-) NEW YORK BLOOD CENTER INC.
PA (CALY) CALIFORNIA INST OF TECHN.
XX
PI Neurath AR, Kent SBH;
XX
DR WPI; 1991-283144/39.
XX
PT Synthetic lipid vesicle carrier linked to pre-S gene coded peptide - the
PT peptide is a hepatitis B immunogen, vaccine or diagnostic.
XX
PS Disclosure; Page 13; 54pp; English.
XX
CC This peptide is one of ten preferred HBV antigenic sequences which are
CC suitable for attachment to lipid vesicles for use as vaccines. The lipid
CC vesicle carrier is stabilised by cross-linking and has covalently bonded
CC sites on its outer surface to bind the peptide. See AAR14086-R14095.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKG 9
|||
Db 9 RKG 11

RESULT 42
AAR26439
ID AAR26439 standard; peptide; 11 AA.
XX
AC AAR26439;
XX
DT 25-MAR-2003 (revised)
DT 08-FEB-1993 (first entry)
XX
DE N-terminal auxiliary sequence.
XX
KW Negative hydrophobicity; increased renaturation yield.
XX
OS Synthetic.
XX
PN EP500108-A2.
XX
PD 26-AUG-1992.
XX
PF 20-FEB-1992; 92EP-00102864.
XX
PR 21-FEB-1991; 91DE-04105480.
XX
PA (BOEFL) BOEHRINGER MANNHEIM GMBH.
XX

PI Ambrosius D, Dony C, Rudolph R;
XX
DR WPI; 1992-286227/35.
XX
PT Increasing denaturation yield of recombinant protein from prokaryotic
PT host - by expressing it with terminal hydrophilic aminoacid sequence
PT attached, pref. detachable at specific cleavage site.
XX
PS Claim 11; Page 14; 18pp; German.
XX
CC The peptide is used as an auxiliary sequence which can be added to the N
CC and/or C-terminus of recombinant proteins which exist in at least
CC partially inactive form and are activated by solubilisation and/or
CC renaturation techniques. The auxiliary sequence has a ratio of relative
CC hydrophobicity:number of amino acids of -2.0 kcal/mole or smaller.
CC Incorporation of the auxiliary sequence increases the yield during the
CC renaturation process. This method is applied to recombinant proteins
CC produced in prokaryotic organisms, especially E. coli. A specific
CC application is production of recombinant granulocyte-colony stimulating
CC factor (GM-CSF) or its derivatives. See also AAR26436-R26444. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 7 GPR 9

RESULT 43
AAR24850
ID AAR24850 standard; protein; 11 AA.
XX
AC AAR24850;
XX
DT 25-MAR-2003 (revised)
DT 08-DEC-1992 (first entry)
XX
DE Weight regulating peptide 33.
XX
KW Amphetamine; appetite suppressor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /label= GLY, ALA, VAL, LEU, SER, THR, CYS, MET, ASP, GLU,
FT ASN, GLN, LYS, HIS, ARG, PHE, TYR, TRP, PRO, OTHER
FT /note= "cystine, hydroxylysine, hydroxyproline"
FT Misc-difference 3
FT /label= GLY, ALA, VAL, LEU, SER, THR, CYS, MET, ASP, GLU,
FT ASN, GLN, LYS, HIS, ARG, PHE, TYR, TRP, PRO, OTHER
FT /note= "cystine, hydroxylysine, hydroxyproline"

XX
PN WO9209296-A1.
XX
PD 11-JUN-1992.
XX
PF 20-NOV-1991; 91WO-US008497.
XX
PR 21-NOV-1990; 90US-00616910.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Fleming PJ, Kent UM;
XX
DR WPI; 1992-216791/26.
XX
PT New dodeca:peptide cpds. - used for regulating wt. gain in mammals or for
PT producing antibodies for attenuating such effects.
XX
PS Disclosure; Page 10; 34pp; English.
XX
CC The sequences given in AAR24818-61 are new peptides which comprise at
CC least 6 amino acids from the sequence given in AAR24814. The remaining
CC amino acids are each Gly, Ala, Val, Leu, Ser, Thr, Cys, cystine, Met,
CC Asp, Glu, Asn, Gln, Lys, hydroxylysine, His, Arg, Phe, Tyr, Trp, Pro or
CC hydroxyproline. These peptides used for the regulation of weight gain in
CC mammals and can be used instead of amphetamine, which is largely used as
CC an appetite suppressor. These peptides can also be used to prepare
CC antibodies. Such antibodies can be used to attenuate the effect of the
CC peptides in a host or to detect, quantify or purify the peptides.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 RKG 9
|||
Db 4 RKG 6

RESULT 44
AAR28129
ID AAR28129 standard; protein; 11 AA.
XX
AC AAR28129;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (17).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Cross-links 4..11
FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg3-Glu-Arg2-Ser-Arg-Gly-Asp-
FT Val sequence (see AAR28128)"
XX
PN WO9208476-A1.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US008328.
XX
PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 40-41; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28128-
CC 29, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 2 RRK 4

RESULT 45
AAR28133
ID AAR28133 standard; protein; 11 AA.
XX
AC AAR28133;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (21).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Cross-links 2..11
FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg-Glu-Arg4-Ser-Arg-Gly-Asp-
FT Val sequence (see AAR28132)"
XX
PN WO9208476-A1.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US008328.
XX
PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 43-44; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28132-
CC 33, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 2 KRR 4

RESULT 46
AAR28088
ID AAR28088 standard; protein; 11 AA.
XX
AC AAR28088;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (13).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Cross-links 6. .11
FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val
FT sequence (see AAR28087)"
XX
PN WO9208476-A1.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US008328.
XX
PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 37-38; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28087-
CC 88, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 4 RRK 6

RESULT 47
AAR28135
ID AAR28135 standard; protein; 11 AA.
XX
AC AAR28135;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (23).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Cross-links 1..11
FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Glu-Arg5-Ser-Arg-Gly-Asp-Val
FT sequence (see AAR28133)"
XX
PN WO9208476-A1.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US008328.
XX
PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 44-45; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28134-
CC 35, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 1 KRR 3

RESULT 48
AAR28090
ID AAR28090 standard; protein; 11 AA.
XX
AC AAR28090;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (15).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Cross-links 5..11
FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg4-Glu-Arg-Ser-Arg-Gly-Asp-
FT Val sequence (see AAR28090)"
XX
PN WO9208476-A1.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US008328.
XX
PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 39-40; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28089-
CC 90, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 3 RRK 5

RESULT 49
AAR28131
ID AAR28131 standard; protein; 11 AA.
XX
AC AAR28131;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (19).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Cross-links 3. .11
FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg2-Glu-Arg3-Ser-Arg-Gly-Asp-
FT Val sequence (see AAR28130)"
XX
PN WO9208476-A1.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US008328.
XX
PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 41-43; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28130-
CC 31, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 1 RRK 3

RESULT 50
AAR27175
ID AAR27175 standard; protein; 11 AA.
XX
AC AAR27175;
XX
DT 25-MAR-2003 (revised)
DT 25-FEB-1993 (first entry)
XX
DE Sequence encoded by anti-Tac(Fab)-PLC.
XX
KW Recombinant immunotoxin; immunosuppressive agent;
KW T-cell mediated disorders; therapy.
XX
OS Synthetic.

XX
PN WO9215327-A1.
XX
PD 17-SEP-1992.
XX
PF 06-MAR-1992; 92WO-US001784.
XX
PR 08-MAR-1991; 91US-00666287.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Chang CN, Queen CL;
XX
DR WPI; 1992-331479/40.
DR N-PSDB; AAQ28938.
XX
PT Recombinant double chain immuno:toxin(s) - for treating e.g. graft versus host disease, auto-immune disease (such as type I diabetes), and malignancies (such as adult T-cell leukaemia).
XX
PS Example; Page 31; 48pp; English.
XX
CC Phospholipase C (PLC), is a highly potent toxin that causes cell damage by hydrolyzing the phospholipid phosphatidylcholine, a major membrane constituent. PLC has been linked to the Fab fragment of the anti-Tac antibody, which recognizes the p55 chain of the human IL-2 receptor to produce an anti-Tac(Fab)-PLC immunotoxin. Anti-Tac(Fab)-PLC specifically binds to and inhibits protein synthesis in human T cells expressing the IL-2 receptor. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 1 KGP 3

RESULT 51
AAR29235
ID AAR29235 standard; peptide; 11 AA.
XX
AC AAR29235;
XX
DT 25-MAR-2003 (revised)
DT 14-APR-1993 (first entry)
XX
DE Heteroconjugate antibody immunogen RP339 (RF).
XX
KW V3 loop; gp41; envelope protein; MN; prototype; virus; variant; HIV;
KW homology; heteroconjugate; enzyme; epitope mapping; replication;
KW conjugate; immunogenic carrier; keyhole limpet hemocyanin; KLH;
KW ovalbumin; succinyl maleimidomethyl cyclohexanylcarboxylate; SMCC.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 11
FT /note= "Not in the natural sequence of this isolate"
XX
PN WO9220373-A1.
XX
PD 26-NOV-1992.
XX
PF 29-APR-1992; 92WO-US003616.
XX
PR 14-MAY-1991; 91US-00699773.
XX
PA (REPK) REPLIGEN CORP.
XX
PI Higgins PJ, Potts BJ;
XX
DR WPI; 1992-415475/50.
XX
PT Hetero-conjugate antibodies for treating HIV infections - comprise an antibody specific for an effector cell surface antigen and an antibody to a V3 loop of GP-120 envelope protein of HIV.

XX
PS Disclosure; Page 19; 69pp; English.
XX

CC The sequences given in AAR29226-35 represent peptides which were used as CC immunogens for the production of antibodies against HIV. These peptides CC may be either unconjugated or conjugated to an immunogenic carrier, eg. a CC keyhole limpet hemocyanin (KLH) or ovalbumin, using succinyl CC maleimidomethyl cyclohexanylcarboxylate (SMCC) as a conjugating agent. CC Viruses containing these or similar sequences may be recognised by the CC heteroconjugate enzymes of the invention. The antibodies raised against CC these sequences may be identified by standard epitope mapping techniques. CC These antibodies are capable, even at low concentrations, of nearly CC eliminating viral replication of different strains of HIV. (Updated on 25 CC -MAR-2003 to correct PN field.)
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 3 KGP 5

RESULT 52
AAR32113
ID AAR32113 standard; protein; 11 AA.
XX
AC AAR32113;
XX
DT 25-MAR-2003 (revised)
DT 28-MAY-1993 (first entry)

XX
DE Light chain CDR1 region for humanised anti-IL-2 receptor antibody.
XX
KW antibody; monoclonal; chimaeric; grafted; humanised; IL-2; interleukin-2;
KW cytokines; interleukin-2 receptor; 55kD beta chain; activated T cells;
KW T cell mediated disease; graft versus host disease; transplant rejection;
KW autoimmune diseases; chemotherapy; immunosuppressants; T cell typing;
KW diagnosis; testing; detection; ss.
XX
OS Rattus rattus.
XX
PN WO9301289-A1.
XX
PD 21-JAN-1993.
XX
PF 10-JUL-1992; 92WO-GB001258.
XX
PR 11-JUL-1991; 91GB-00015010.
XX
PA (WELL) WELLCOME FOUND LTD.
PA (WALD/) WALDMANN H.
XX
PI Waldmann H, Winter GP, Crowe JS, Lewis AP;
XX
DR WPI; 1993-045493/05.
DR N-PSDB; AAQ36574.
XX
PT Human interleukin-2 receptor antibodies - useful for treating and
PT preventing T-cell mediated diseases e.g. graft versus host disease,
PT transplant rejection etc.
XX
PS Claim 1; Page 26; 48pp; English.
XX
CC This sequence represents the light chain CDR1 region from rat monoclonal
CC antibody YTH 906.9.25 which binds to the 55kD beta-chain of the IL-2
CC receptor on activated T cells. The encoding DNA was used in the
CC construction of humanised anti-IL2 receptor by PCR methods using CAMPATH-
CC 1H L chain as light chain template, and a humanised anti-CD4 heavy chain
CC as a template. The humanised anti-IL2 receptor Ab can be used in the
CC treatment of T-cell mediated diseases eg. graft versus host disease,
CC transplant rejection, and various autoimmune diseases. It may be
CC administered alone or with chemotherapeutic or immunosuppressive agents.
CC In addn. it can be used for T cell typing, to isolate specific IL-2R
CC bearing cells and for diagnosis. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 53
AAR32411
ID AAR32411 standard; peptide; 11 AA.
XX
AC AAR32411;
XX
DT 25-MAR-2003 (revised)
DT 04-JUL-1993 (first entry)
XX
DE Sequence of peptide B6 which comprises AAs 327-337 from the V3 region of
DE HIV-1 isolate RF.
XX
KW HIV-1; vaccine; dendritic core; ss.
XX
OS Synthetic.
XX
PN WO9303766-A1.
XX
PD 04-MAR-1993.
XX
PF 11-AUG-1992; 92WO-US006688.
XX
PR 13-AUG-1991; 91US-00744281.
XX
PA (REPK) REPLIGEN CORP.
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Tam JP, Profy AT;
XX
DR WPI; 1993-093730/11.
XX
PT New multiple antigen peptide(s) as HIV vaccines - include a dendritic
PT core covalently bonded to peptide including the sequence IGPGR.
XX
PS Example; Fig 1; 35pp; English.
XX
CC Nine peptides from the V3 regions of HIV-1 isolates IIIb, RF and MN were
CC incorporated into tetravalent multiple antigen peptide systems (MAPS)
CC (see AAR32406-14). Parallel groups of three peptides with chain lengths
CC spanning from 11-24 residues were synthesised in MAPS formate for each
CC isolate. ELIS assays demonstrated that antisera titers in mice were
CC closely related to the length of the IIIb peptide used for the
CC immunisation - the longer the stronger the response. There was no
CC substantial antibody prodn. in mice against the other two series of
CC peptides, RF (B4-B6), and MN (B7-B9), except for a low reactivity in the
CC gp. immunised with B8 (MN isolate). Specificity tests of the B cell
CC response demonstrated that the T cell epitope (AAR32415) also serves as a
CC B cell epitope. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||

RESULT 54

AAR33224

ID AAR33224 standard; peptide; 11 AA.

XX

AC AAR33224;

XX

DT 25-MAR-2003 (revised)

DT 13-JUL-1993 (first entry)

XX

DE HIV gp120 V3 loop immunogenic peptide RP339 (RF).

XX

KW HIV-1; human immunodeficiency virus; antibody generation; AIDS;

KW infection; CD4 binding site; soluble CD4.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 11

FT /note= "not in natural sequence of isolate"

XX

PN WO9304693-A1.

XX

PD 18-MAR-1993.

XX

PF 02-SEP-1992; 92WO-US007511.

XX

PR 09-SEP-1991; 91US-00756677.

PR 20-JUL-1992; 92US-00916542.

XX

PA (REPK) REPLIGEN CORP.

XX

PI Potts BJ, Whitescharf ME, Field KG, Herlihy WC;

XX

DR WPI; 1993-100653/12.

XX

PT Synergistic compsn. for treating HIV-1 infection - comprises antibody to
PT V3 loop of GP120 and antibody to CD4 binding site of GP120 or soluble CD4
PT polypeptide.

XX

PS Example; Page 12; 56pp; English.

XX

CC The sequence is that of peptide RP339 (RF) used as an immunogen for the
CC generation of antibodies directed against the V3 loop of HIV gp120. These
CC antibodies can be used as part of a compsn. with antibodies directed
CC against the CD4 binding site of gp120. The antibodies act synergistically
CC to neutralise HIV-1 in the treatment of HIV infection caused by different
CC strains. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR
CC -2003 to correct PI field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 3 KGP 5

RESULT 55
AAR32352
ID AAR32352 standard; peptide; 11 AA.
XX
AC AAR32352;
XX
DT 05-JUL-1993 (first entry)
XX
DE Human Factor X peptide.
XX
KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin; formation; Factor Xa; pathway mediated activation; inhibition.
XX
OS Synthetic.
XX
PN US5187155-A.
XX
PD 16-FEB-1993.
XX
PF 23-JUN-1989; 89US-00371561.
XX
PR 23-JUN-1989; 89US-00371561.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Fair DS;
XX
DR WPI; 1993-075751/09.
XX
PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit factor X activation and/or Factor Xa function, useful for preventing blood clot formation and treating deep vein thrombosis, pulmonary embolism, etc.
XX
PS Example; Page 6; 23pp; English.
XX
CC The sequence is that of a peptide corresponding to amino acids 404-414 of the human factor X molecule which was tested for its effect, (as a % of the control rate), on the rate of Factor Xa formation and on the rate of thrombin formation. The results obtd. were for activation of Factor X by the extrinsic activation complex 78%, by the intrinsic activation complex 98%, and activation by RVV-X, 76%. For the rate of thrombin formation the rate was 88% as compared to the control rate
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKG 9

RESULT 56
AAR46532
ID AAR46532 standard; peptide; 11 AA.
XX
AC AAR46532;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1994 (first entry)
XX
DE Myelin basic protein sequence.
XX
KW Autoimmunity; polar lipid; targetting; immune response;
KW antigenic peptide; antigen.
XX
OS Synthetic.
XX
PN US5256641-A.
XX
PD 26-OCT-1993.
XX
PF 09-JUL-1992; 92US-00911209.
XX
PR 01-NOV-1990; 90US-00607982.
XX
PA (OREG-) STATE OF OREGON.
XX
PI Yatvin MB, Stowell MHB, Malkovsky M;
XX
DR WPI; 1993-350862/44.
XX
PT New covalent conjugate of antigenic peptide and polar lipid e.g.
PT sphingosine - useful in protective vaccines, treatment of auto-immune
PT disease and preventing of transplant rejection.
XX
PS Disclosure; Page 13; 15pp; English.
XX
CC The peptide is an example of an antigenic peptide which may be joined via
CC a functional linker group, opt. at the two ends of a spacer group, to a
CC polar lipid carrier, e.g. sphingosine, ceramide, phosphatidyl choline,
CC ethanolamine, inositol or serine, cardiolipin or phosphatidic acid. The
CC compsn. may be used to alleviate autoimmune diseases. An advantage of the
CC carrier system is that when incorporated into the compsn. entry of the
CC antigenic peptide into the cells of the immune system is facilitated (no
CC need for endocytosis) and targetting to specific organelles becomes
CC possible. Unlike known vaccines, intracellular synthesis of viral
CC antigens is not necessary for presentation via the MHC class I antigen
CC pathway, nor intracellular proteolysis for presentation via the MHC class
CC II antigen pathway, so both humoral and cellular immunity is achieved.
CC Also, when a spacer is present, the antigen release rate may be
CC controlled. See also AAR46507-47. (Updated on 25-MAR-2003 to correct PF
CC field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASQ 3
|||
Db 1 ASQ 3

RESULT 57

AAR38680

ID AAR38680 standard; peptide; 11 AA.

XX

AC AAR38680;

XX

DT 25-MAR-2003 (revised)

DT 01-NOV-1993 (first entry)

XX

DE Bradykinin antagonist (4).

XX

KW Oedema; pancreas; enzyme; acute pancreatitis; serum amylase; lipase;

KW hypovolaemia; hyperalbuminaemia; pain.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "(4-benzoyl)benzoyl-Lys"

FT Misc-difference 2

FT /note= "D-form residue"

FT Modified-site 5

FT /note= "hydroxyproline"

FT Modified-site 7

FT /note= "2-thienylalanine"

FT Modified-site 9

FT /note= "D-1,2,3,4 tetrahydroisoquinoline-3-yl-carbonyl"

FT Modified-site 10

FT /note= "cis, endo octahydroindolecarbonyl"

XX

PN EP548825-A1.

XX

PD 30-JUN-1993.

XX

PF 18-DEC-1992; 92EP-00121558.

XX

PR 21-DEC-1991; 91EP-00122055.

XX

PA (FARH) HOECHST AG.

XX

PI Griesbacher T, Lembeck F;

XX

DR WPI; 1993-206998/26.

XX

PT Compsn. to treat acute pancreatitis - comprising peptide(s) as bradykinin antagonists.

XX

PS Claim 4; Page 11; 16pp; English.

XX

CC This sequence is an example of a highly generic formula. The peptide is a
CC bradykinin antagonist which prevents bradykinin-induced oedema and thus
CC allows pancreatic enzymes to leave the tissue without hindrance. The
CC peptide is useful in the treatment of acute pancreatitis which is
CC characterised by a massive oedema of the gland and the retroperitoneal
CC tissue, interstitial activation of proteolytic enzymes, elevation of
CC serum amylase and lipase levels, hypovolaemia, hyperalbuminaemia,
CC pulmonary oedema and severe pain. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 1 KRR 3

RESULT 58

AAR40877

ID AAR40877 standard; protein; 11 AA.

XX

AC AAR40877;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-MAR-1994 (first entry)

XX

DE SSP for flavonoid-3',5'-hydroxylase gene product.

XX

KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression; ss.

XX

OS Petunia x hybrida.

XX

PN WO9318155-A1.

XX

PD 16-SEP-1993.

XX

PF 20-NOV-1992; 92WO-JP001520.

XX

PR 02-MAR-1992; 92JP-00044963.

XX

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.

XX

PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;

XX

DR WPI; 1993-303469/38.

DR N-PSDB; AAQ47878.

XX

PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 58; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 5 GPR 7

RESULT 59
AAR41632
ID AAR41632 standard; protein; 11 AA.
XX
AC AAR41632;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX
PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;

XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47882.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 60; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 5 GPR 7

RESULT 60
AAR40880
ID AAR40880 standard; protein; 11 AA.
XX
AC AAR40880;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-MAR-1994 (first entry)
XX
DE SSP for flavonoid-3',5'-hydroxylase gene product.
XX
KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;
KW polymerase chain reaction; amplification; expression.
XX
OS Petunia x hybrida.
XX
PN WO9318155-A1.
XX
PD 16-SEP-1993.
XX
PF 20-NOV-1992; 92WO-JP001520.
XX
PR 02-MAR-1992; 92JP-00044963.
XX

PA (KYOW) KYOWA HAKKO KOGYO CO LTD.
XX
PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;
PI Okinaka Y;
XX
DR WPI; 1993-303469/38.
DR N-PSDB; AAQ47881.
XX
PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to
PT transform plants e.g. petunia, rose or tobacco to give bluer flower
PT colour and altered pigment pattern.
XX
PS Claim 11; Page 59; 82pp; Japanese.
XX
CC Insertion of the sequences (AAQ47840-42) into plants such as rose,
CC petunia, tobacco and carnation, using a suitable vector such as
CC agrobacterium, give transformed plants which express the gene, resulting
CC in petals with a bluer colour than normal, and/or pigmentation patterns
CC which do not occur naturally. The sequences were amplified using primers
CC (AAQ47843-70). Related single specific primers using a gene sequence
CC coding for the haem-binding region of cytochrome P450 are shown in
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 5 GPR 7

RESULT 61
AAR37602
ID AAR37602 standard; peptide; 11 AA.
XX
AC AAR37602;
XX
DT 25-MAR-2003 (revised)
DT 13-OCT-1993 (first entry)
XX
DE hIL2R Ab L chain V region CDR1.
XX
KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
KW region; PCR; framework; plasmid.
XX
OS Mus musculus.
XX
PN WO9311238-A1.
XX
PD 10-JUN-1993.
XX

PF 03-DEC-1992; 92WO-JP001583.
XX
PR 06-DEC-1991; 91JP-00323319.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (BIOT) BIOTEST PHARMA GMBH.
PA (INNO-) INNOTHERAPIE LAB.
XX
PI Nakatani T, Gomi H, Wijdenes J, Noguchi H;
XX
DR WPI; 1993-197057/24.
XX
PT Humanised antibody comprising - CDR region of mouse MAB B-B10 specific
PT for IL-2 receptor useful for treating carcinoma expressing IL-2 receptor.
XX
PS Claim 1; Page 42; 62pp; English.
XX
CC The sequences given in AAR37599-604 represent the complementarity-
CC determining regions (CDRs) of a humanised antibody (Ab) which binds
CC specifically to human interleukin (IL)-2 receptor (hIL2R). These CDRs
CC were derived from the murine anti-human IL-2 receptor monoclonal Ab (MAb)
CC B-B10 (see also AAQ43242-43). This MAb is antagonistic to the binding of
CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human
CC mixed lymphocyte reaction. The cDNA encoding the variable (V) region of
CC the B-B10 Ab was cloned by PCR and sequenced (see also AAQ43226-32 and
CC AAQ43233-36). A human Ab with high levels of amino acid sequence homology
CC to the murine sequence was selected and the framework of this Ab was
CC bound with the B-B10 V region CDR and a part of the framework to design
CC several kinds of the humanised B-B10 V region (see also AAQ43244-45). The
CC DNA sequence coding this humanised B-B10 was synthesised and a plasmid
CC expressing humanised B-B10 was constructed. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 62
AAR42981
ID AAR42981 standard; peptide; 11 AA.
XX
AC AAR42981;
XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1994 (first entry)
XX
DE MHC class I binding peptide (Db-restricted).
XX
KW MHC; binding peptide; T-cell immunity; conjugate; carbohydrate;
KW major histocompatibility complex; tumour.

XX
OS Synthetic.
XX
PN WO9321948-A1.
XX
PD 11-NOV-1993.
XX
PF 23-APR-1993; 93WO-SE000353.
XX
PR 28-APR-1992; 92SE-00001338.
PR 07-SEP-1992; 92SE-00002553.
PR 23-DEC-1992; 92SE-00003897.
PR 06-APR-1993; 93SE-00001141.
XX
PA (ASTR) ASTRA AB.
XX
PI Jondal M;
XX
DR WPI; 1993-368417/46.
XX
PT New peptide-carbohydrate conjugate stimulating T cell immunity - specific
PT for carbohydrate component, for control of tumours and infectious
PT diseases, by generating cytotoxic T cells.
XX
PS Disclosure; Page 40; 109pp; English.
XX
CC Immunogenic conjugates useful for generating T-cell immunity against
CC tumour-associated carbohydrate structures or against carbohydrate
CC structures expressed on infectious agents and/or infected host cells
CC comprise (i) a peptide component capable of binding a MHC class I mol.;
CC and (ii) a carbohydrate component having the immunogenic specificity of
CC the carbohydrate structure. Examples capable of binding MHC class I mols.
CC in the murine system are given in AAR42988- 89, which are both presented
CC by H-2-Db mols. An example of a peptide capable of binding an MHC class I
CC mol. in the human system is given in AAR42983, which is presented by HLA-
CC A2.1 mols. Examples of peptides suitable for conjugation are given in
CC AAR42966-87. Conjugation of a MHC class II binding peptide (AAR42990) to
CC a carbohydrate is described in Elofsson et al., (1991), Tetrahedron Lett.
CC 32, 7613-7616. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 1 KGP 3

RESULT 63
AAR62885
ID AAR62885 standard; peptide; 11 AA.
XX
AC AAR62885;
XX

DT 25-MAR-2003 (revised)
DT 18-JUL-1995 (first entry)
XX
DE Murine anti-human atherosclerotic plaque MAb Z2D3 VK CDR1.
XX
KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
KW murine monoclonal antibody; kappa light chain variable region: CDR1;
KW complementarity determining region; imaging; plaque ablation.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1. .11
FT /label= CDR1
XX
PN WO9425053-A1.
XX
PD 10-NOV-1994.
XX
PF 26-APR-1994; 94WO-US004641.
XX
PR 26-APR-1993; 93US-00053451.
XX
PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
XX
PI Ditlow CC, Chen FW, Calenoff E;
XX
DR WPI; 1994-357904/44.
DR N-PSDB; AAQ78740.
XX
PT New antigen comprising hydroxy:steroid and quat. ammonium salt - and
PT related antibodies, useful e.g. for imaging, ablating or treating
PT atherosclerotic plaque, and detecting plaque specific antibodies.
XX
PS Claim 201; Page 164; 288pp; English.
XX
CC Mice were immunised with an extract of human atherosclerotic plaque, then
CC spleen cells were fused with SP2/01-Ag-14 myeloma cells. Hybridomas were
CC screened by ELISA for reactivity with the immunogen and clone Z2D3 was
CC isolated. The Z2D3 antibody reacts specifically with atherosclerotic
CC tissue; it recognises a non-protein antigen containing cholesterol (or
CC similar steroid that is a substrate for cholesterol oxidase) and a
CC quaternary ammonium salt (pref. a phosphatidylcholine or related compound
CC that is a substrate for phospholipase C). The CDR sequences for the heavy
CC and light chains of Z2D3 were determined; peptides comprising the CDRs
CC are claimed, including chimeric (CDR-grafted) murine-human antibodies.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 64
AAR67043
ID AAR67043 standard; peptide; 11 AA.
XX
AC AAR67043;
XX
DT 25-MAR-2003 (revised)
DT 29-JUN-1995 (first entry)
XX
DE Granulocyte colony stimulating peptide (GCSP-1) contg. proline brackets.
XX
KW colony stimulating peptide; growth promoter; treatment; neutropenia;
KW proliferation; differentiation; constrained conformation; mimic;
KW interaction site.
XX
OS Synthetic.
XX
PN WO9425482-A1.
XX
PD 10-NOV-1994.
XX
PF 21-APR-1994; 94WO-US004294.
XX
PR 23-APR-1993; 93US-00051741.
PR 29-OCT-1993; 93US-00143364.
XX
PA (EVAN/) EVANS H J.
PA (KINI/) KINI R M.
XX
PI Evans HJ, Kini RM;
XX
DR WPI; 1994-358186/44.
XX
PT Peptide homologue or analogue with constrained conformation - has proline
PT residues flanking the interaction site to impart greater, or more stable,
PT biological activity.
XX
PS Example 2; Page 26; 57pp; English.
XX
CC AAR67043-48 are granulocyte colony stimulating peptides (GCSP) derived
CC from naturally occurring polypeptides that contain proline or
CC proline/cysteine brackets. These peptides are shortened to form fragments
CC that contain one or more interaction sites of interest. AAR67043-47
CC originate from GCSP which interacts with specific receptors. GCSP is
CC helpful in proliferation and differentiation of haemopoietic precursors
CC and stimulation of mature cells. It is also used for treatment of
CC neutropenia in a variety of clinical situations. Dose is 50-200
CC nanomoles. The data collected demonstrates that interaction sites possess
CC activity when present in a polypeptide that differs from the native form.
CC Inclusion of conformation-constraining moieties can have desirable
CC effects on an interaction site. (Also see AAR67011-42 and AAR67049-152
CC for analogues of other biologically active peptides contg. an interaction
CC site flanked by conformation constraining gps., eg. RGD peptides.)
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4
|||
Db 3 SQA 5

RESULT 65

AAR66140

ID AAR66140 standard; peptide; 11 AA.

XX

AC AAR66140;

XX

DT 12-JUL-1995 (first entry)

XX

DE CD-4 antibody variable region complementary peptide.

XX

KW CD-4 antibody variable region; complementary peptide;

KW extra-corporeal blood circulation; cell filter material.

XX

OS Synthetic.

XX

PN JP06269663-A.

XX

PD 27-SEP-1994.

XX

PF 17-MAR-1993; 93JP-00057206.

XX

PR 17-MAR-1993; 93JP-00057206.

XX

PA (TOYM) TOYOB KK.

XX

DR WPI; 1994-346316/43.

XX

PT Material for collecting cells positive for CD-4 antibody - comprises
PT nonwoven fabric having keto-alkyl halide functional gp.

XX

PS Disclosure; Page 3; 9pp; Japanese.

XX

CC AAR66140-R66146 are peptides complementary to the variable region of the
CC CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric
CC (average fibre dia. of 1-30 microns) coated with keto-alkyl halide
CC functional groups. This material can be used as a filter for CD-4
CC positive cells in a medical treatment involving the extra-corporeal
CC circulation of blood

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3

Db

|||
2 ASQ 4

RESULT 66

AAR65955

ID AAR65955 standard; peptide; 11 AA.

XX

AC AAR65955;

XX

DT 25-MAR-2003 (revised)

DT 03-AUG-1995 (first entry)

XX

DE N-terminal peptide of recombinant cholesterol oxidase.

XX

KW cholesterol oxidase; enzymatic test; assay; cholesterol determination;

KW high affinity; cytoplasmic enzyme; signal peptide.

XX

OS Synthetic.

XX

PN WO9425603-A1.

XX

PD 10-NOV-1994.

XX

PF 02-MAY-1994; 94WO-EP001394.

XX

PR 05-MAY-1993; 93DE-04314793.

PR 09-DEC-1993; 93DE-04342012.

XX

PA (BOEUF) BOEHRINGER MANNHEIM GMBH.

XX

PI Jarsch M;

XX

DR WPI; 1994-358279/44.

DR N-PSDB; AAQ78263.

XX

PT New cholesterol oxidase from *Brevibacterium sterolicum* - and related DNA
PT and recombinant enzyme, useful for cholesterol assay, has high
PT cholesterol affinity and can be produced in large amts. as cytoplasmic
PT enzyme.

XX

PS Claim 7; Page 29; 83pp; German.

XX

CC AAR65952-7 show the N-terminal peptide sequences of recombinant
CC cholesterol oxidase, and replace the native signal peptide sequence.
CC These heterologous signal sequences are encoded by AAQ78259-63, and the
CC full length recombinant sequences are shown in AAR65958-63 (encoded by
CC AAQ78265-70). Recombinant cholesterol oxidases are useful in cholesterol
CC assays, as the enzyme has high cholesterol affinity and can be produced
CC in large amts. as a cytoplasmic enzyme. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 8 KRR 10

RESULT 67
AAR52526
ID AAR52526 standard; peptide; 11 AA.
XX
AC AAR52526;
XX
DT 10-OCT-1996 (first entry)
XX
DE 3D6 light chain complementarity determining region 1.
XX
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify; anti-phenylarsonate antibody.
XX
OS Synthetic.
XX
PN EP592106-A1.
XX
PD 13-APR-1994.
XX
PF 07-SEP-1993; 93EP-00307051.
XX
PR 09-SEP-1992; 92US-00942245.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Pedersen JT, Searle SMJ, Rees AR, Roguska MA, Guild BC;
XX
DR WPI; 1994-120230/15.
XX
PT Method of resurfacing of rodent antibodies to produce humanised antibody
PT forms - for producing non human antibodies with improved therapeutic
PT efficiency by presenting human surface on V-region.
XX
PS Example 2; Page 31; 230pp; English.
XX
CC The predicted structures of 4 different antibody (Gloop-2 and D1.3, anti-
CC lysozyme Abs; 36-71, an anti-phenylarsonate Ab; and 3D6, an anti- protein
CC (GP41 of HIV) Ab) Fv regions were analysed. This information can be used
CC in a method to determine how to modify a rodent antibody or fragment by
CC resurfacing in order to produce a humanised rodent antibody. Global fits
CC give a more realistic measure of the accuracy of the model than a local
CC least-squares fit over the loops since they account for the overall
CC positioning of the loops in the context of the Fv structure. Differences
CC between local and global Root Mean Square deviations arise from
CC differences in VH/VL domain packing and differences in loop "take off"
CC angles and positions. AAR52523-46 are the peptide sequences of the 24
CC CDRs
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 68
AAR52523
ID AAR52523 standard; peptide; 11 AA.
XX
AC AAR52523;
XX
DT 10-OCT-1996 (first entry)
XX
DE Gloop-2 light chain complementarity determining region 1.
XX
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify; anti-phenylarsonate antibody.
XX
OS Synthetic.
XX
PN EP592106-A1.
XX
PD 13-APR-1994.
XX
PF 07-SEP-1993; 93EP-00307051.
XX
PR 09-SEP-1992; 92US-00942245.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Pedersen JT, Searle SMJ, Rees AR, Roguska MA, Guild BC;
XX
DR WPI; 1994-120230/15.
XX
PT Method of resurfacing of rodent antibodies to produce humanised antibody
PT forms - for producing non human antibodies with improved therapeutic
PT efficiency by presenting human surface on V-region.
XX
PS Example 2; Page 31; 230pp; English.
XX
CC The predicted structures of 4 different antibody (Gloop-2 and D1.3, anti-
CC lysozyme Abs; 36-71, an anti-phenylarsonate Ab; and 3D6, an anti- protein
CC (GP41 of HIV) Ab) Fv regions were analysed. This information can be used
CC in a method to determine how to modify a rodent antibody or fragment by
CC resurfacing in order to produce a humanised rodent antibody. Global fits
CC give a more realistic measure of the accuracy of the model than a local
CC least-squares fit over the loops since they account for the overall
CC positioning of the loops in the context of the Fv structure. Differences
CC between local and global Root Mean Square deviations arise from
CC differences in VH/VL domain packing and differences in loop "take off"
CC angles and positions. AAR52523-46 are the peptide sequences of the 24
CC CDRs

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 69
AAR52525
ID AAR52525 standard; peptide; 11 AA.
XX
AC AAR52525;
XX
DT 10-OCT-1996 (first entry)
XX
DE 36-71 light chain complementarity determining region 1.
XX
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify; anti-phenylarsonate antibody.
XX
OS Synthetic.
XX
PN EP592106-A1.
XX
PD 13-APR-1994.
XX
PF 07-SEP-1993; 93EP-00307051.
XX
PR 09-SEP-1992; 92US-00942245.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Pedersen JT, Searle SMJ, Rees AR, Roguska MA, Guild BC;
XX
DR WPI; 1994-120230/15.
XX
PT Method of resurfacing of rodent antibodies to produce humanised antibody
PT forms - for producing non human antibodies with improved therapeutic
PT efficiency by presenting human surface on V-region.
XX
PS Example 2; Page 31; 230pp; English.
XX
CC The predicted structures of 4 different antibody (Gloop-2 and D1.3, anti-
CC lysozyme Abs; 36-71, an anti-phenylarsonate Ab; and 3D6, an anti- protein
CC (GP41 of HIV) Ab) Fv regions were analysed. This information can be used
CC in a method to determine how to modify a rodent antibody or fragment by
CC resurfacing in order to produce a humanised rodent antibody. Global fits
CC give a more realistic measure of the accuracy of the model than a local
CC least-squares fit over the loops since they account for the overall
CC positioning of the loops in the context of the Fv structure. Differences
CC between local and global Root Mean Square deviations arise from

CC differences in VH/VL domain packing and differences in loop "take off"
CC angles and positions. AAR52523-46 are the peptide sequences of the 24
CC CDRs

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 70

AAR85774

ID AAR85774 standard; peptide; 11 AA.

XX

AC AAR85774;

XX

DT 19-JAN-1996 (first entry)

XX

DE L-CDR-1 of anti-idiotype antibody against human anticancer antibody.

XX

KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.

XX

OS Mus sp.

XX

PN JP07101999-A.

XX

PD 18-APR-1995.

XX

PF 06-OCT-1993; 93JP-00272950.

XX

PR 06-OCT-1993; 93JP-00272950.

XX

PA (HAGI/) HAGIWARA Y.

XX

DR WPI; 1995-182987/24.

XX

PT Novel anti-idiotype antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.

XX

PS Claim 11; Page 4; 28pp; Japanese.

XX

CC A new anti-idiotype antibody against a human anticancer monoclonal
CC antibody is claimed. This antibody contains in its heavy chain 3
CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2 (AAR74932
CC -R74935) and CDR3 (AAR74936-R74939), this is also true of the light
CC chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
CC encoding it are useful in pharmacological, medical and biochemical fields

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 71
AAR74946
ID AAR74946 standard; peptide; 11 AA.
XX
AC AAR74946;
XX
DT 19-JAN-1996 (first entry)
XX
DE L-CDR-1 of anti-idiotype antibody against human anticancer antibody.
XX
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN JP07101999-A.
XX
PD 18-APR-1995.
XX
PF 06-OCT-1993; 93JP-00272950.
XX
PR 06-OCT-1993; 93JP-00272950.
XX
PA (HAGI/) HAGIWARA Y.
XX
DR WPI; 1995-182987/24.
XX
PT Novel anti-idiotype antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
XX
PS Claim 11; Page 4; 28pp; Japanese.
XX
CC A new anti-idiotype antibody against a human anticancer monoclonal
CC antibody is claimed. This antibody contains in its heavy chain 3
CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2 (AAR74932
CC -R794935) and CDR3 (AAR74936-R74939), this is also true of the light
CC chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
CC encoding it are useful in pharmacological, medical and biochemical fields
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 72
AAR85157
ID AAR85157 standard; protein; 11 AA.
XX
AC AAR85157;
XX
DT 18-JAN-1996 (first entry)
XX
DE Human ONS-M21 antibody light variable region CDR 1.
XX
KW Human; ONS-M21 antibody; light variable region; chimeric protein;
KW complementarity determining region; CDR 1; medulloblastoma; brain tumour;
KW treatment; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9514041-A1.
XX
PD 26-MAY-1995.
XX
PF 19-OCT-1994; 94WO-JP001763.
XX
PR 19-NOV-1993; 93JP-00291078.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Sato K, Tsuchiya M;
XX
DR WPI; 1995-200347/26.
XX
PT Reconstituted antibody against human medulloblastoma cells - contains
PT high proportion of human antibody origin and has low antigenicity.
XX
PS Claim 1; Page 100; 120pp; Japanese.
XX
CC AAR85157-R85159 are human antibody ONS-M21 light variable region
CC complementarity determining regions (CDRs). They were used in the
CC construction of a human/murine chimeric antibody, reactive with human
CC medulloblastoma (a brain tumour) cells. The chimeric antibody can be used
CC in the diagnosis and treatment of this disease
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 73
AAW21496

ID AAW21496 standard; peptide; 11 AA.

XX

AC AAW21496;

XX

DT 16-OCT-2003 (revised)

DT 30-JUL-1997 (first entry)

XX

DE Hepatitis delta antigen derived signal oligopeptide #1.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;

KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;

KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;

KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;

KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;

KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;

KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;

KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;

KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;

KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;

KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Hepatitis D virus.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as regions of max. hydrophilicity, used in modulating communication between protein(s).

XX

PS Claim 5; Page 72; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligopeptides. These signal oligopeptides are localised on the surface of the protein and are represented by the hydrophilicity maxima of the protein. These peptides are enriched in charged amino acids arranged with neutral spacer amino acids. The specific signal character of these oligopeptides is determined by a characteristic combination of conformation and charge within the signal sequence. These oligopeptides may be used as vaccines in the treatment of human disease, as competitive inhibitors to prevent or reduce the metabolic action or interaction of a selected protein by blocking its specific signal sequences, or as therapeutic agents to function as feedback regulators to reduce synthesis rate of a selected protein. These peptides may be modified by omitting one or more amino

CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RRK 8
|||
Db 2 RRK 4

RESULT 74

AAW21470

ID AAW21470 standard; peptide; 11 AA.

XX

AC AAW21470;

XX

DT 30-JUL-1997 (first entry)

XX

DE Collagenase (fibroblast MMP1) derived signal oligopeptide #2.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between

PT protein(s).

XX

PS Claim 5; Page 68; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligopeptides. These signal oligopeptides are localised on the surface of the protein and are represented by the hydrophilicity maxima of the protein. CC These peptides are enriched in charged amino acids arranged with neutral CC spacer amino acids. The specific signal character of these oligopeptides CC is determined by a characteristic combination of conformation and charge CC within the signal sequence. These oligopeptides may be used as vaccines CC in the treatment of human disease, as competitive inhibitors to prevent CC or reduce the metabolic action or interaction of a selected protein by CC blocking its specific signal sequences, or as therapeutic agents to CC function as feedback regulators to reduce synthesis rate of a selected CC protein. These peptides may be modified by omitting one or more amino CC acids at the N- and/or C-terminal, by substituting one or more amino CC acids without consideration of charge and polarity, by substituting one CC or more amino acids with amino acid residues with similar charge and/or CC polarity, by omitting one or more amino acids or a combination of these

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7

|||

Db 9 KRR 11

RESULT 75

AAW21329

ID AAW21329 standard; peptide; 11 AA.

XX

AC AAW21329;

XX

DT 29-JUL-1997 (first entry)

XX

DE Glucagon precursor derived signal oligopeptide #34.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US000575.
XX
PR 14-JAN-1994; 94US-00182248.
XX
PA (RATH/) RATH M.
XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).
XX
PS Claim 5; Page 44; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 9 AKR 11

Search completed: April 8, 2004, 15:40:05
Job time : 47.3077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
(without alignments)
50.221 Million cell updates/sec

Title: US-09-787-443A-15

Perfect score: 11

Sequence: 1 ASQAKRRKGPR 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	4	36.4	11	1	US-08-378-859-4	Sequence 4, Appli
2	4	36.4	11	2	US-08-669-721-17	Sequence 17, Appli
3	4	36.4	11	2	US-08-540-388-1	Sequence 1, Appli
4	4	36.4	11	2	US-08-348-353-3	Sequence 3, Appli
5	4	36.4	11	2	US-08-465-965-3	Sequence 3, Appli
6	4	36.4	11	3	US-08-465-966-3	Sequence 3, Appli
7	4	36.4	11	3	US-08-970-648-4	Sequence 4, Appli
8	4	36.4	11	3	US-09-189-344-17	Sequence 17, Appli
9	4	36.4	11	4	US-09-839-743-20	Sequence 20, Appli
10	4	36.4	11	4	US-08-952-558-1	Sequence 1, Appli
11	4	36.4	11	5	PCT-US92-10068-7	Sequence 7, Appli

12	4	36.4	11	5	PCT-US95-11127-16	Sequence 16, Appl
13	3	27.3	11	1	US-08-155-171B-42	Sequence 42, Appl
14	3	27.3	11	1	US-08-155-171B-43	Sequence 43, Appl
15	3	27.3	11	1	US-08-139-054-5	Sequence 5, Appli
16	3	27.3	11	1	US-08-318-970B-14	Sequence 14, Appl
17	3	27.3	11	1	US-08-318-970B-15	Sequence 15, Appl
18	3	27.3	11	1	US-08-481-888A-20	Sequence 20, Appl
19	3	27.3	11	1	US-07-942-245-494	Sequence 494, App
20	3	27.3	11	1	US-07-942-245-496	Sequence 496, App
21	3	27.3	11	1	US-07-942-245-497	Sequence 497, App
22	3	27.3	11	1	US-07-942-245-518	Sequence 518, App
23	3	27.3	11	1	US-07-942-245-522	Sequence 522, App
24	3	27.3	11	1	US-08-485-273A-20	Sequence 20, Appl
25	3	27.3	11	1	US-08-445-745-119	Sequence 119, App
26	3	27.3	11	1	US-08-445-745-153	Sequence 153, App
27	3	27.3	11	1	US-08-349-902B-30	Sequence 30, Appl
28	3	27.3	11	1	US-08-687-226-69	Sequence 69, Appl
29	3	27.3	11	1	US-08-277-660A-12	Sequence 12, Appl
30	3	27.3	11	1	US-08-548-540-118	Sequence 118, App
31	3	27.3	11	1	US-08-548-540-121	Sequence 121, App
32	3	27.3	11	1	US-08-329-820-106	Sequence 106, App
33	3	27.3	11	1	US-08-329-820-199	Sequence 199, App
34	3	27.3	11	1	US-08-649-272A-1	Sequence 1, Appli
35	3	27.3	11	1	US-08-424-957-25	Sequence 25, Appl
36	3	27.3	11	1	US-08-137-117D-117	Sequence 117, App
37	3	27.3	11	1	US-08-633-760-14	Sequence 14, Appl
38	3	27.3	11	1	US-08-054-860-11	Sequence 11, Appl
39	3	27.3	11	2	US-08-480-434-66	Sequence 66, Appl
40	3	27.3	11	2	US-08-480-434-75	Sequence 75, Appl
41	3	27.3	11	2	US-08-480-434-76	Sequence 76, Appl
42	3	27.3	11	2	US-08-436-717-117	Sequence 117, App
43	3	27.3	11	2	US-08-669-721-18	Sequence 18, Appl
44	3	27.3	11	2	US-08-669-721-21	Sequence 21, Appl
45	3	27.3	11	2	US-08-669-721-22	Sequence 22, Appl
46	3	27.3	11	2	US-08-762-695-1	Sequence 1, Appli
47	3	27.3	11	2	US-08-468-819-14	Sequence 14, Appl
48	3	27.3	11	2	US-08-318-157B-20	Sequence 20, Appl
49	3	27.3	11	2	US-08-637-759B-479	Sequence 479, App
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51	3	27.3	11	2	US-08-232-081B-4	Sequence 4, Appli
52	3	27.3	11	2	US-08-973-559-20	Sequence 20, Appl
53	3	27.3	11	2	US-08-934-222-36	Sequence 36, Appl
54	3	27.3	11	2	US-08-435-998-42	Sequence 42, Appl
55	3	27.3	11	2	US-08-435-998-43	Sequence 43, Appl
56	3	27.3	11	2	US-08-933-402-36	Sequence 36, Appl
57	3	27.3	11	2	US-09-207-621-36	Sequence 36, Appl
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59	3	27.3	11	2	US-08-053-451B-75	Sequence 75, Appl
60	3	27.3	11	2	US-08-053-451B-76	Sequence 76, Appl
61	3	27.3	11	2	US-08-706-741B-54	Sequence 54, Appl
62	3	27.3	11	2	US-08-476-176B-53	Sequence 53, Appl
63	3	27.3	11	2	US-08-532-818-36	Sequence 36, Appl
64	3	27.3	11	2	US-08-602-725-6	Sequence 6, Appli
65	3	27.3	11	2	US-08-482-228-48	Sequence 48, Appl
66	3	27.3	11	2	US-08-924-695A-54	Sequence 54, Appl
67	3	27.3	11	3	US-08-856-074A-37	Sequence 37, Appl
68	3	27.3	11	3	US-08-592-500-38	Sequence 38, Appl

69	3	27.3	11	3	US-08-592-500-39	Sequence 39, Appl
70	3	27.3	11	3	US-08-592-500-40	Sequence 40, Appl
71	3	27.3	11	3	US-08-871-355A-479	Sequence 479, App
72	3	27.3	11	3	US-08-482-528-48	Sequence 48, Appl
73	3	27.3	11	3	US-08-442-378-11	Sequence 11, Appl
74	3	27.3	11	3	US-08-159-339A-1139	Sequence 1139, Ap
75	3	27.3	11	3	US-08-127-721A-53	Sequence 53, Appl
76	3	27.3	11	3	US-08-485-246A-53	Sequence 53, Appl
77	3	27.3	11	3	US-08-195-006-38	Sequence 38, Appl
78	3	27.3	11	3	US-08-195-006-39	Sequence 39, Appl
79	3	27.3	11	3	US-08-195-006-40	Sequence 40, Appl
80	3	27.3	11	3	US-09-231-797-36	Sequence 36, Appl
81	3	27.3	11	3	US-08-599-226-7	Sequence 7, Appli
82	3	27.3	11	3	US-08-894-173-4	Sequence 4, Appli
83	3	27.3	11	3	US-08-934-224-36	Sequence 36, Appl
84	3	27.3	11	3	US-09-105-799-1	Sequence 1, Appli
85	3	27.3	11	3	US-08-933-843-36	Sequence 36, Appl
86	3	27.3	11	3	US-08-649-100-11	Sequence 11, Appl
87	3	27.3	11	3	US-08-649-100-27	Sequence 27, Appl
88	3	27.3	11	3	US-08-816-346-14	Sequence 14, Appl
89	3	27.3	11	3	US-08-934-223-36	Sequence 36, Appl
90	3	27.3	11	3	US-08-679-006-13	Sequence 13, Appl
91	3	27.3	11	3	US-09-035-686-25	Sequence 25, Appl
92	3	27.3	11	3	US-09-335-411-14	Sequence 14, Appl
93	3	27.3	11	3	US-09-273-565-54	Sequence 54, Appl
94	3	27.3	11	3	US-08-915-314-19	Sequence 19, Appl
95	3	27.3	11	3	US-08-915-314-44	Sequence 44, Appl
96	3	27.3	11	3	US-09-189-344-18	Sequence 18, Appl
97	3	27.3	11	3	US-09-189-344-21	Sequence 21, Appl
98	3	27.3	11	3	US-09-189-344-22	Sequence 22, Appl
99	3	27.3	11	3	US-09-398-193-4	Sequence 4, Appli
100	3	27.3	11	3	US-08-646-265A-118	Sequence 118, App

ALIGNMENTS

RESULT 1

US-08-378-859-4

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; Sequence 4, Application US/08378859
; Patent No. 5728553
; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R
; APPLICANT: Sleep, Darrell
; APPLICANT: van Urk, Hendrik
; APPLICANT: Berezenko, Stephen
; APPLICANT: Woodrow, John R
; APPLICANT: Johnson, Richard A
; APPLICANT: Wood, Patricia C
; APPLICANT: Burton, Steven J
; APPLICANT: Quirk, Alan V
; TITLE OF INVENTION: High Purity Albumin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill, New Providence
```

; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,859
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H8501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 771 6292
; TELEFAX: (908) 771 6159
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Peptide fragment of human serum albumin
US-08-378-859-4

Query Match 36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
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Db 4 ASQA 7

RESULT 2
US-08-669-721-17
; Sequence 17, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA

; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-669-721-17

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
|||
Db 2 AKRR 5

RESULT 3

US-08-540-388-1

; Sequence 1, Application US/08540388
; Patent No. 5858964
; GENERAL INFORMATION:
; APPLICANT: AHARONI, Rina
; APPLICANT: ARNON, Ruth
; APPLICANT: CHAO, Nelson J.
; APPLICANT: SCHLEGEL, Paul G.
; APPLICANT: SELA, Michael
; APPLICANT: TEITELBAUM, Dvora
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SYNTHETIC PEPTIDE COPOLYMER FOR PREVENTION OF GVHD
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,388
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/421,412
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AHARONI=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: The alanine at position 1 is acetylated
US-08-540-388-1

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
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Db 1 ASQA 4

RESULT 4
US-08-348-353-3
; Sequence 3, Application US/08348353
; Patent No. 5932217
; GENERAL INFORMATION:
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Masure, Robert
; TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
; TITLE OF INVENTION: Ligand for Leukocyte CR3
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,353
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson, David
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-097CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-348-353-3

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
|||
Db 4 QAKR 7

RESULT 5
US-08-465-965-3
; Sequence 3, Application US/08465965
; Patent No. 5968512
; GENERAL INFORMATION:
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Masure, Robert
; TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
; TITLE OF INVENTION: Ligand for Leukocyte CR3
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,965

; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/348,353
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/247,572
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03725
; FILING DATE: 04-MAY-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/695,613
; FILING DATE: 03-MAY-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson, David
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-097CIP1DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-965-3

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
|||
Db 4 QAKR 7

RESULT 6
US-08-465-966-3
; Sequence 3, Application US/08465966
; Patent No. 6015560
; GENERAL INFORMATION:
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Masure, Robert
; TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
; TITLE OF INVENTION: Ligand for Leukocyte CR3
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack

; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,966
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/348,353
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/247,572
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03725
; FILING DATE: 04-MAY-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/695,613
; FILING DATE: 03-MAY-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson, David
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-097CIP1DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-966-3

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
 ||||
Db 4 QAKR 7

RESULT 7
US-08-970-648-4
; Sequence 4, Application US/08970648
; Patent No. 6034221

; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R
; APPLICANT: Sleep, Darrell
; APPLICANT: van Urk, Hendrik
; APPLICANT: Berezenko, Stephen
; APPLICANT: Woodrow, John R
; APPLICANT: Johnson, Richard A
; APPLICANT: Wood, Patricia C
; APPLICANT: Burton, Steven J
; APPLICANT: Quirk, Alan V
; TITLE OF INVENTION: High Purity Albumin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill, New Providence
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,648
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378,859
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H8501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 771 6292
; TELEFAX: (908) 771 6159
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Peptide fragment of human serum albumin
US-08-970-648-4

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 ASQA 4

Db ||||
4 ASQA 7

RESULT 8
US-09-189-344-17
; Sequence 17, Application US/09189344
; Patent No. 6191258
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/669,721
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-189-344-17

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
Db ||||
2 AKRR 5

RESULT 9

US-09-839-743-20

; Sequence 20, Application US/09839743
; Patent No. 6472211
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

US-09-839-743-20

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
||||
Db 2 AKRR 5

RESULT 10

US-08-952-558-1

; Sequence 1, Application US/08952558
; Patent No. 6638740
; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R.
; APPLICANT: Sleep, Darrell
; APPLICANT: Berezenko, Stephen
; APPLICANT: Woodrow, John R.
; APPLICANT: Johnson, Richard A.
; TITLE OF INVENTION: PROCESS OF HIGH PURITY ALBUMIN PRODUCTION
; FILE REFERENCE: CE0111D US
; CURRENT APPLICATION NUMBER: US/08/952,558
; CURRENT FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: PCT/GB96/00449
; PRIOR FILING DATE: 1996-02-29
; PRIOR APPLICATION NUMBER: 378,859
; PRIOR FILING DATE: 1995-05-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-952-558-1

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
||||
Db 4 ASQA 7

RESULT 11
PCT-US92-10068-7
; Sequence 7, Application PC/TUS9210068
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C
; APPLICANT: Edgington, Thomas S
; APPLICANT: Fair, Daryl S
; TITLE OF INVENTION: Factor X-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic
Methods
; TITLE OF INVENTION: for Inhibiting Inflammation
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10068
; FILING DATE: 19921120
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,221
; FILING DATE: 22-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: SCR1221P
; REFERENCE/DOCKET NUMBER: 34,163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1
; OTHER INFORMATION: /note= "Added amino-terminal
; OTHER INFORMATION: glycine residue"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note= "Added carboxy-terminal
; OTHER INFORMATION: glycine residue"
PCT-US92-10068-7

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAKR 6
 ||||
Db 4 QAKR 7

RESULT 12

PCT-US95-11127-16

; Sequence 16, Application PC/TUS9511127
; GENERAL INFORMATION:
; APPLICANT: ROBERT WEBBER
; TITLE OF INVENTION: DOPAMINE RECEPTOR PEPTIDES AND
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIELEN, PETERSON & LAMPE
; STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720
; CITY: WALNUT CREEK
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE 5.25 INCH, 1.2 MB FOR FORMATTED
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11127
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NONE
; FILING DATE: NONE
; ATTORNEY/AGENT INFORMATION:
; NAME: THEODORE J. BIELEN, JR.
; REGISTRATION NUMBER: 27,420
; REFERENCE/DOCKET NUMBER: 12068

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 937-1515
; TELEFAX: (510) 937-1529
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; NAME/KEY: D3 RECEPTOR (22-32)
; LOCATION:
; IDENTIFICATION METHOD: AMINO ACID ANALYSIS
; OTHER INFORMATION: DOPAMINE D3 RECEPTOR PEPTIDE
PCT-US95-11127-16

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
 ||||
Db 2 ASQA 5

RESULT 13
US-08-155-171B-42
; Sequence 42, Application US/08155171B
; Patent No. 5543264
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Mangel, Walter F.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,171B
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/851,217
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/545,585
; FILING DATE: 29-JUN-1990

; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-155-171B-42

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 6 KRR 8

RESULT 14

US-08-155-171B-43

; Sequence 43, Application US/08155171B
; Patent No. 5543264
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Mangel, Walter F.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,171B
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/851,217
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/545,585
; FILING DATE: 29-JUN-1990

; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-155-171B-43

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 6 KRR 8

RESULT 15

US-08-139-054-5

; Sequence 5, Application US/08139054
; Patent No. 5578710
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothea
; APPLICANT: Dony, Carola
; APPLICANT: Rudolph, Rainer
; TITLE OF INVENTION: IMPROVED ACTIVATION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 1725 K. St. N.W. Suite 1000
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/139,054
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/837,779
; FILING DATE:
; APPLICATION NUMBER: DE P 41 05 480.6
; FILING DATE: 21-FEB-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: 920053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-139-054-5

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
 |||
Db 7 GPR 9

RESULT 16
US-08-318-970B-14
; Sequence 14, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL
ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: L CDR1-3
; OTHER INFORMATION: hypervariable region
US-08-318-970B-14

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 17

US-08-318-970B-15

; Sequence 15, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL
ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: L CDR1-4
; OTHER INFORMATION: hypervariable region
US-08-318-970B-15

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 18
US-08-481-888A-20
; Sequence 20, Application US/08481888A
; Patent No. 5631228
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Roberts, F. Donald
; TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL
; TITLE OF INVENTION: HISTATIN-BASED PEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,888A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/287,717
; FILING DATE: 09-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,030
; FILING DATE: 28-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,571
; FILING DATE: 01-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-481-888A-20

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
 |||
Db 1 AKR 3

RESULT 19

US-07-942-245-494

; Sequence 494, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 494:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-494

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 20

US-07-942-245-496

; Sequence 496, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 496:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-496

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 21

US-07-942-245-497
; Sequence 497, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 497:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-497

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 22
US-07-942-245-518
; Sequence 518, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 518:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-518

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 23
US-07-942-245-522
; Sequence 522, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.

; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 522:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-522

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 24
US-08-485-273A-20
; Sequence 20, Application US/08485273A
; Patent No. 5646119
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciapoli, Peter
; TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,273A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/287,717
; FILING DATE: 09-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,030
; FILING DATE: 28-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,571
; FILING DATE: 01-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..11
; OTHER INFORMATION: /note= "At least one amino acid
; OTHER INFORMATION: must have a D configuration."
US-08-485-273A-20

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 1 AKR 3

RESULT 25
US-08-445-745-119
; Sequence 119, Application US/08445745
; Patent No. 5672585
; GENERAL INFORMATION:

; APPLICANT: Pierschbacher, Michael D.
; APPLICANT: Cheng, Soan
; APPLICANT: Craig, William S.
; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: Methods and Composition for Treating
; TITLE OF INVENTION: Thrombosis
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,745
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,068
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/079,441
; FILING DATE: 18-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,73614
; FILING DATE: 14-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-445-745-119

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKG 9
|||

RESULT 26
US-08-445-745-153
; Sequence 153, Application US/08445745
; Patent No. 5672585
; GENERAL INFORMATION:
; APPLICANT: Pierschbacher, Michael D.
; APPLICANT: Cheng, Soan
; APPLICANT: Craig, William S.
; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: Methods and Composition for Treating
; TITLE OF INVENTION: Thrombosis
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,745
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,068
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/079,441
; FILING DATE: 18-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,73614
; FILING DATE: 14-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: circular

; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 2
; OTHER INFORMATION: /note= "Xaa = (Pmc)"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 8
; OTHER INFORMATION: /note= "Xaa = (Y-OMe)"
US-08-445-745-153

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 3 GPR 5

RESULT 27
US-08-349-902B-30
; Sequence 30, Application US/08349902B
; Patent No. 5674839
; GENERAL INFORMATION:
; APPLICANT: Victor J. Hruby et al
; TITLE OF INVENTION: Linear and Cyclic Analogs of
; TITLE OF INVENTION: alpha-MSH fragments
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,902B
; FILING DATE: 6-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: UA 816 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: cyclic

; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: position 2 is
; OTHER INFORMATION: No. 5674839leucine; position 5 is D-phenylalanine
US-08-349-902B-30

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 8 KGP 10

RESULT 28

US-08-687-226-69

; Sequence 69, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-226-69

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
 |||
Db 4 GPR 6

RESULT 29

US-08-277-660A-12

; Sequence 12, Application US/08277660A

; Patent No. 5702908

; GENERAL INFORMATION:

; APPLICANT: Picksley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,660A

; FILING DATE: 20-JUL-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-60244/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-277-660A-12

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SQA 4
|||
Db 1 SQA 3

RESULT 30

US-08-548-540-118

; Sequence 118, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/548,540
; FILING DATE: 26-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-548-540-118

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 31

US-08-548-540-121

; Sequence 121, Application US/08548540

; Patent No. 5733731

; GENERAL INFORMATION:

; APPLICANT: Schatz, Peter J.

; APPLICANT: Cull, Millard G.

; APPLICANT: Miller, Jeff F.

; APPLICANT: Stemmer, Willem P.C.

; APPLICANT: Gates, Christian M.

; TITLE OF INVENTION: Peptide Library and Screening Method

; NUMBER OF SEQUENCES: 162

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: William M. Smith

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/548,540

; FILING DATE: 26-OCT-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/290,641

; FILING DATE: 15-AUG-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/963,321

; FILING DATE: 15-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 16528J-001240US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 121:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-548-540-121

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 1 KRR 3

RESULT 32

US-08-329-820-106

; Sequence 106, Application US/08329820
; Patent No. 5747457
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: FELDING-HABERMANN, BRUNHILDE
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: RIPPmann, FRIEDRICH
; TITLE OF INVENTION: Linear Adhesion Inhibitors
; NUMBER OF SEQUENCES: 228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,820
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4336758.5
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1635
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "Cys(Trt)"
; FEATURE:
; NAME/KEY: Modified-site

; LOCATION: 3
; OTHER INFORMATION: /product= "Arg(Mtr)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Asn(Trt)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /product= "His(Trt)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /product= "Lys(Boc)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "Thr(But)-OMe"
US-08-329-820-106

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 7 KGP 9

RESULT 33
US-08-329-820-199
; Sequence 199, Application US/08329820
; Patent No. 5747457
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: FELDING-HABERMANN, BRUNHILDE
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: RIPPmann, FRIEDRICH
; TITLE OF INVENTION: Linear Adhesion Inhibitors
; NUMBER OF SEQUENCES: 228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,820
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4336758.5
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1635
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "X is A"
; OTHER INFORMATION: /note= "A is as defined"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /product= "Cys(R1)"
; OTHER INFORMATION: /note= "R1 is as defined"
US-08-329-820-199

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 8 KGP 10

RESULT 34
US-08-649-272A-1
; Sequence 1, Application US/08649272A
; Patent No. 5763393
; GENERAL INFORMATION:
; APPLICANT: MOSKAL, Joseph R
; APPLICANT: YAMAMOTO, Hirotaka
; APPLICANT: COLLEY, Patricia A
; TITLE OF INVENTION: Neuroactive Peptides
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,272A

; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,1204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "NT-1"

US-08-649-272A-1

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 35

US-08-424-957-25

; Sequence 25, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown

US-08-424-957-25

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4
|||
Db 1 SQA 3

RESULT 36
US-08-137-117D-117
; Sequence 117, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-137-117D-117

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 37

US-08-633-760-14

; Sequence 14, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: FUJIMURA, TAKAO
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: NOGUCHI, YUJI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,760
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-929-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-633-760-14

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 5 RRK 7

RESULT 38
US-08-054-860-11
; Sequence 11, Application US/08054860
; Patent No. 5807559
; GENERAL INFORMATION:
; APPLICANT: Jondal, Mikael
; TITLE OF INVENTION: New Active Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,860
; FILING DATE: 19930427
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9201338-2
; FILING DATE: 28-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202553-5
; FILING DATE: 07-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203897-5
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301141-9
; FILING DATE: 06-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J
; REGISTRATION NUMBER: P-35, 372
; REFERENCE/DOCKET NUMBER: 1103326
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-054-860-11

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
 |||
Db 1 KGP 3

RESULT 39

US-08-480-434-66

; Sequence 66, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-480-434-66

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 40

US-08-480-434-75

; Sequence 75, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N

US-08-480-434-75

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 41

US-08-480-434-76

; Sequence 76, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N

US-08-480-434-76

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 42

US-08-436-717-117

; Sequence 117, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-436-717-117

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 43

US-08-669-721-18

; Sequence 18, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-669-721-18

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 44

US-08-669-721-21

; Sequence 21, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-721-21

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 4 KRR 6

RESULT 45

US-08-669-721-22

; Sequence 22, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-721-22

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 4 KRR 6

RESULT 46

US-08-762-695-1

; Sequence 1, Application US/08762695
; Patent No. 5846738
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, CHRISTOPH
; APPLICANT: BIALK, PETER
; APPLICANT: VON DER ELTZ, HERBERT
; TITLE OF INVENTION: SYNTHETIC STANDARD FOR IMMUNOASSAYS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM
; STREET: METROPOLITAN SQUARE, 655 15TH ST, N.W., SUITE
; STREET: 330-G ST.Lobby
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,695
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/325,589
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: DE P 43 35 798.9
; FILING DATE: 20-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 17 735.6
; FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 20 742.5
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NOLAN, SHARON L.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: P1614.4050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-762-695-1

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 7 KRR 9

RESULT 47

US-08-468-819-14

; Sequence 14, Application US/08468819
; Patent No. 5871723
; GENERAL INFORMATION:
; APPLICANT: Strieter, Robert M.
; APPLICANT: Polverini, Peter J.
; APPLICANT: Kunkel, Steven L.
; TITLE OF INVENTION: CXC Chemokines as Regulators of
; TITLE OF INVENTION: Angiogenesis
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,819
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-468-819-14

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKG 9
|||
Db 5 RKG 7

RESULT 48

US-08-318-157B-20

; Sequence 20, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-318-157B-20

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3

Db

|||
2 ASQ 4

RESULT 49

US-08-637-759B-479

; Sequence 479, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 479:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

US-08-637-759B-479

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3

|||

Db 7 ASQ 9

RESULT 50

US-08-973-563A-20

; Sequence 20, Application US/08973563A
; Patent No. 5885965

; GENERAL INFORMATION:

; APPLICANT: Oppenheim, Frank G.

; APPLICANT: Xu, Tao

; APPLICANT: Spacciapoli, Peter

; APPLICANT: Roberts, F. D.

; APPLICANT: Friden, Philip M.

; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based

; TITLE OF INVENTION: Peptides

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: US

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/973,563A

; FILING DATE: 07-JUN-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/485,273

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.

; REGISTRATION NUMBER: 22,592

; REFERENCE/DOCKET NUMBER: PER95-02A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 781-861-6240

; TELEFAX: 781-861-9540

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..11

; OTHER INFORMATION: /note= "At least one amino acid

; OTHER INFORMATION: must have a D configuration."

US-08-973-563A-20

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 1 AKR 3

RESULT 51

US-08-232-081B-4

; Sequence 4, Application US/08232081B

; Patent No. 5886152

; GENERAL INFORMATION:

; APPLICANT: NAKATANI, TOMOYUKI

; APPLICANT: GOMI, HIDEYUKI

; APPLICANT: WIJDENES, JOHN

; APPLICANT: NOGUCHI, HIROSHI

; TITLE OF INVENTION: HUMANIZED B-B10

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

; STREET: PO BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,081B

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: SVENSSON, LEONARD R

; REGISTRATION NUMBER: 30,330

; REFERENCE/DOCKET NUMBER: 20-3484

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 205-8000

; TELEFAX: (703) 205-8050

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-232-081B-4

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 52
US-08-973-559-20
; Sequence 20, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-973-559-20

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
 |||
Db 1 AKR 3

RESULT 53
US-08-934-222-36
; Sequence 36, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-934-222-36

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4
|||
Db 3 SQA 5

RESULT 54
US-08-435-998-42
; Sequence 42, Application US/08435998
; Patent No. 5935840
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Mangel, Walter F.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,998
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,171
; FILING DATE: 19-NOV-1993
; APPLICATION NUMBER: US 07/851,217
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/545,585
; FILING DATE: 29-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-998-42
Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||

RESULT 55
US-08-435-998-43
; Sequence 43, Application US/08435998
; Patent No. 5935840
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Mangel, Walter F.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,998
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,171
; FILING DATE: 19-NOV-1993
; APPLICATION NUMBER: US 07/851,217
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/545,585
; FILING DATE: 29-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-998-43

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 6 KRR 8

RESULT 56
US-08-933-402-36
; Sequence 36, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-933-402-36

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4

Db

|||
3 SQA 5

RESULT 57
US-09-207-621-36
; Sequence 36, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction Sit
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-36

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 SQA 4

|||
Db 3 SQA 5

RESULT 58
US-08-053-451B-66
; Sequence 66, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451B-66

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 59
US-08-053-451B-75
; Sequence 75, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451B-75

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 60
US-08-053-451B-76
; Sequence 76, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451B-76

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 61
US-08-706-741B-54

; Sequence 54, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMAYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAVERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-706-741B-54

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 62

US-08-476-176B-53

; Sequence 53, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype

; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-476-176B-53

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 63
US-08-532-818-36
; Sequence 36, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-36

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQA 4
|||
Db 3 SQA 5

RESULT 64
US-08-602-725-6
; Sequence 6, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DURBIN, HELGA
; APPLICANT: SNARY, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: VL chain CDR1

US-08-602-725-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 65
US-08-482-228-48
; Sequence 48, Application US/08482228
; Patent No. 5968753

; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-482-228-48

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 7 ASQ 9

RESULT 66

US-08-924-695A-54

; Sequence 54, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAVERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-924-695A-54

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 67

US-08-856-074A-37

; Sequence 37, Application US/08856074A
; Patent No. 6004798
; GENERAL INFORMATION:
; APPLICANT: Anderson, W. French
; APPLICANT: Wu, Bonnie W.
; TITLE OF INVENTION: Retroviral Envelopes Having
; TITLE OF INVENTION: Modified Hypervariable polyproline Regions
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey

; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,074A
; FILING DATE: 14-May-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-378
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide

US-08-856-074A-37

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 1 GPR 3

RESULT 68

US-08-592-500-38

; Sequence 38, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: GPV thrombin cleavage site."
FEATURE:
; NAME/KEY: Region
; LOCATION: 1..2
; OTHER INFORMATION: /note= "Amino acid residues found
; OTHER INFORMATION: in other thrombin substrates."
FEATURE:
; NAME/KEY: Region
; LOCATION: 5..9
; OTHER INFORMATION: /note= "Amino acid residues found
; OTHER INFORMATION: in other thrombin substrates."
FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note= "Amino acid residue found in
; OTHER INFORMATION: other thrombin substrates."
US-08-592-500-38

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 5 GPR 7

US-08-592-500-39

; Sequence 39, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: human fibrinogen (Fg) A-alpha 1 chain thrombin
; OTHER INFORMATION: cleavage site."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..2
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "Amino acid residue

; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..9
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
US-08-592-500-39

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 8 GPR 10

RESULT 70

US-08-592-500-40

; Sequence 40, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: human fibrinogen (Fg) A-alpha 2 chain thrombin
; OTHER INFORMATION: cleavage site."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5..7
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
US-08-592-500-40

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 5 GPR 7

RESULT 71
US-08-871-355A-479
; Sequence 479, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-479

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 7 ASQ 9

RESULT 72

US-08-482-528-48

; Sequence 48, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-482-528-48

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 7 ASQ 9

RESULT 73

US-08-442-378-11

; Sequence 11, Application US/08442378
; Patent No. 6033669
; GENERAL INFORMATION:
; APPLICANT: Jondal, Mikael
; TITLE OF INVENTION: New Active Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,378
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/054,860
; FILING DATE: 27-APR-1993
; APPLICATION NUMBER: SE 9201338-2
; FILING DATE: 28-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202553-5
; FILING DATE: 07-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203897-5
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301141-9

; FILING DATE: 06-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J
; REGISTRATION NUMBER: P-35, 372
; REFERENCE/DOCKET NUMBER: 1103326
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-442-378-11

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 1 KGP 3

RESULT 74

US-08-159-339A-1139

; Sequence 1139, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1139

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 8 GPR 10

RESULT 75
US-08-127-721A-53
; Sequence 53, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-127-721A-53

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

Search completed: April 8, 2004, 15:52:12
Job time : 12.3077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
(without alignments)
122.816 Million cell updates/sec

Title: US-09-787-443A-15

Perfect score: 11

Sequence: 1 ASQAKRRKGPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	3	27.3	11	2	A40693	transgelin - sheep
2	3	27.3	11	2	S00616	parasporal crystal
3	3	27.3	11	2	PT0302	Ig heavy chain CRD
4	3	27.3	11	2	S57575	T cell receptor V-
5	3	27.3	11	2	A33571	follistatin - bovi
6	2	18.2	11	1	XAVIBH	bradykinin-potenti
7	2	18.2	11	1	XASNBA	bradykinin-potenti
8	2	18.2	11	2	A33917	dihydroorotate (EC
9	2	18.2	11	2	JN0023	substance P - chic
10	2	18.2	11	2	S32575	ribosomal protein
11	2	18.2	11	2	A38841	rhodopsin homolog
12	2	18.2	11	2	A26930	ermG leader peptid
13	2	18.2	11	2	B26744	megascoliakinin -

14	2	18.2	11	2	S23308	substance P - rain
15	2	18.2	11	2	S23306	substance P - Atla
16	2	18.2	11	2	S07201	physalaemin - frog
17	2	18.2	11	2	F58501	43.5K bile stone p
18	2	18.2	11	2	JQ0395	hypothetical prote
19	2	18.2	11	2	S66606	quinoline 2-oxidor
20	2	18.2	11	2	S42587	celF protein - Esc
21	2	18.2	11	2	B43669	hypothetical prote
22	2	18.2	11	2	D60691	phycobilisome 9K 1
23	2	18.2	11	2	PC2372	58K heat shock pro
24	2	18.2	11	2	E41476	probable antigen 5
25	2	18.2	11	2	H54346	pyruvate synthase
26	2	18.2	11	2	S70338	napin small chain
27	2	18.2	11	2	G61497	seed protein ws-23
28	2	18.2	11	2	S19775	wound-induced prot
29	2	18.2	11	2	PU0029	33K protein 3218 -
30	2	18.2	11	2	PS0259	39K protein 3225 -
31	2	18.2	11	2	S78026	ribosomal protein
32	2	18.2	11	2	A34135	DNA-binding protei
33	2	18.2	11	2	A26120	6-phosphofructokin
34	2	18.2	11	2	B60769	Ig H2 chain - Paci
35	2	18.2	11	2	S33300	probable substance
36	2	18.2	11	2	S43626	cytochrome-c oxida
37	2	18.2	11	2	C37196	bradykinin-potenti
38	2	18.2	11	2	D37196	bradykinin-potenti
39	2	18.2	11	2	E57789	gallbladder stone
40	2	18.2	11	2	I54193	Rhesus blood group
41	2	18.2	11	2	D56979	collagen alpha 1(I
42	2	18.2	11	2	A14454	6-phosphofructokin
43	2	18.2	11	2	PH1632	Ig H chain V-D-J r
44	2	18.2	11	2	PH1583	Ig H chain V-D-J r
45	2	18.2	11	2	PH1375	T antigen variant
46	2	18.2	11	2	PH1376	T antigen variant
47	2	18.2	11	2	PT0217	T-cell receptor be
48	2	18.2	11	2	C38887	T-cell receptor ga
49	2	18.2	11	2	I41946	T-cell receptor ga
50	2	18.2	11	2	PD0441	translation elonga
51	2	18.2	11	2	S53436	beta-D-galactosida
52	2	18.2	11	2	S65377	cytochrome-c oxida
53	2	18.2	11	2	PH0939	T-cell receptor be
54	2	18.2	11	2	PH0940	T-cell receptor be
55	2	18.2	11	2	PH0941	T-cell receptor be
56	2	18.2	11	2	PH0929	T-cell receptor be
57	2	18.2	11	2	PH0891	T-cell receptor be
58	2	18.2	11	2	PH0938	T-cell receptor be
59	2	18.2	11	2	PH0947	T-cell receptor be
60	2	18.2	11	2	PH0903	T-cell receptor be
61	2	18.2	11	2	PH0904	T-cell receptor be
62	2	18.2	11	2	PH0924	T-cell receptor be
63	2	18.2	11	2	PH0919	T-cell receptor be
64	2	18.2	11	2	PH0914	T-cell receptor be
65	2	18.2	11	2	PH0922	T-cell receptor be
66	2	18.2	11	2	PH0906	T-cell receptor be
67	2	18.2	11	2	S60294	tubulin 2 beta-3 c
68	2	18.2	11	4	S19015	hypothetical prote
69	2	18.2	11	4	I54081	retinoic acid rece
70	1	9.1	11	1	ECLQ2M	tachykinin II - mi

71	1	9.1	11	1	SPHO	substance P - hors
72	1	9.1	11	1	EOOCC	eledoisin - curled
73	1	9.1	11	1	A60654	substance P - guin
74	1	9.1	11	1	EOOC	eledoisin - musky
75	1	9.1	11	1	GMROL	leucosulfakinin -
76	1	9.1	11	1	LFTWWE	probable trpEG lea
77	1	9.1	11	2	S66196	alcohol dehydrogen
78	1	9.1	11	2	G42762	proteasome endopep
79	1	9.1	11	2	S68392	H+-transporting tw
80	1	9.1	11	2	B49164	chromogranin-B - r
81	1	9.1	11	2	PQ0682	photosystem I 17.5
82	1	9.1	11	2	C53652	rhlR protein - Pse
83	1	9.1	11	2	S09074	cytochrome P450-4b
84	1	9.1	11	2	A57458	gene Gax protein -
85	1	9.1	11	2	D60409	kassinin-like pept
86	1	9.1	11	2	F60409	substance P-like p
87	1	9.1	11	2	E60409	substance P-like p
88	1	9.1	11	2	YHRT	morphogenetic neur
89	1	9.1	11	2	YHHU	morphogenetic neur
90	1	9.1	11	2	YHBO	morphogenetic neur
91	1	9.1	11	2	YHXAE	morphogenetic neur
92	1	9.1	11	2	YHJFHY	morphogenetic neur
93	1	9.1	11	2	A61365	phyllokinin - Rohd
94	1	9.1	11	2	B60409	kassinin-like pept
95	1	9.1	11	2	C60409	kassinin-like pept
96	1	9.1	11	2	S07203	uperolein - frog (
97	1	9.1	11	2	S07207	Crinia-angiotensin
98	1	9.1	11	2	A61033	ranatachykinin A -
99	1	9.1	11	2	D61033	ranatachykinin D -
100	1	9.1	11	2	S42449	ant1 protein - pha

ALIGNMENTS

RESULT 1

A40693

transgelin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.

J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.

A;Reference number: A40693; MUID:93273790; PMID:8501116

A;Accession: A40693

A;Molécule type: protein

A;Residues: 1-11 <SHA>

A;Experimental source: aorta

C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.

C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology

C;Keywords: actin binding; cytoskeleton

Query Match

27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KGP 10
|||
Db 1 KGP 3

RESULT 2
S00616
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleriae 11-67) (fragment)
N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C;Species: Bacillus thuringiensis
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996
C;Accession: S00616
R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A;Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.
A;Reference number: S00615
A;Accession: S00616
A;Molecule type: protein
A;Residues: 1-11 <CHE>
C;Comment: This toxin is effective against the larvae of Galleria melonella (greater wax moth) but not those of Lymantria dispar (gypsy moth).
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4
|||
Db 9 SQA 11

RESULT 3
PT0302
Ig heavy chain CRD3 region (clone 5-112) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0302
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0302
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 3 GPR 5

RESULT 4
S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is
diversified by tolerance to a background MHC antigen.
A;Reference number: S57494
A;Accession: S57575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <BUR>
A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C;Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 5
A33571
follistatin - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993
C;Accession: A33571
R;Gospodarowicz, D.; Lau, K.
Biochem. Biophys. Res. Commun. 165, 292-298, 1989
A;Title: Pituitary follicular cells secrete both vascular endothelial growth
factor and follistatin.
A;Reference number: A33571; MUID:90073725; PMID:2590228
A;Accession: A33571
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <GOS>

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QAK 5
|||

Db

7 QAK 9

RESULT 6

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive;

bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10

||

Db 6 GP 7

RESULT 7

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 8

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 7 KG 8

RESULT 9

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 10

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)
C;Species: plastid Conopholis americana (squawroot)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
C;Accession: S32575
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of
photosynthesis in a lineage of parasitic plants.
A;Reference number: S32575; MUID:92145776; PMID:1723664
A;Accession: S32575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <TAY>
A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C;Genetics:
A;Gene: rps2
A;Genome: plastid
C;Superfamily: Escherichia coli ribosomal protein S2
C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 3 RR 4

RESULT 11

A38841

rhodopsin homolog - squid (Watasenia scintillans) (fragment)
N;Alternate names: visual pigment protein
C;Species: Watasenia scintillans (sparkling enope)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997
C;Accession: A38841
R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
Biochim. Biophys. Acta 957, 318-321, 1988
A;Title: Amino acid sequence of the retinal binding site of squid visual
pigment.
A;Reference number: PT0063; MUID:89051045; PMID:3191148
A;Accession: A38841
A;Molecule type: protein
A;Residues: 1-11 <SEI>
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; retinal

F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 2 AK 3

RESULT 12

A26930

ermG leader peptide 1 - *Bacillus sphaericus*

C;Species: *Bacillus sphaericus*

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882

C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 6 KR 7

RESULT 13

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: *Megascolia flavifrons* (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp *Megascolia flavifrons*.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of *Megascolia flavifrons*.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein
A;Residues: 1-11 <NAK>
C;Superfamily: unassigned animal peptides
C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 9 RK 10

RESULT 14

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 15

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23306
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 16
S07201
physalaemin - frog (*Physalaemus fuscomaculatus*)
C;Species: *Physalaemus fuscomaculatus*
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07201
R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.
Experientia 20, 489-490, 1964
A;Title: Structure and pharmacological actions of physalaemin, the main active polypeptide of the skin of *Physalaemus fuscumaculatus*.
A;Reference number: S07201; MUID:66076612; PMID:5857249
A;Accession: S07201
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 1 QA 2

RESULT 17
F58501
43.5K bile stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: F58501

R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: F58501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>
A;Experimental source: human bile with stones
A;Note: 6-Asn and 8-Ala were also found

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 8 GP 9

RESULT 18
JQ0395
hypothetical protein (nodB 3' region) - Azorhizobium caulinodans
N;Alternate names: hypothetical 1.4K protein
C;Species: Azorhizobium caulinodans
A;Note: host Sesbania rostrata
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994
C;Accession: JQ0395
R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.
Mol. Genet. 219, 289-298, 1989
A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:
nucleotide sequence and plant-inducible expression.
A;Reference number: JQ0393; MUID:90136519; PMID:2615763
A;Accession: JQ0395
A;Molecule type: DNA
A;Residues: 1-11 <GOE>
A;Cross-references: GB:L18897
A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 2 RR 3

RESULT 19
S66606
quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66606
R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5

||

Db 1 AK 2

RESULT 20

S42587

celf protein - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995

C;Accession: S42587

R;Guzzo, A.; DuBow, M.S.

Mol. Genet. 242, 455-460, 1994

A;Title: A luxAB transcriptional fusion to the cryptic celf gene of Escherichia coli displays increased luminescence in the presence of nickel.

A;Reference number: S42587; MUID:94166755; PMID:8121401

A;Accession: S42587

A;Molecule type: DNA

A;Residues: 1-11 <GUZ>

C;Genetics:

A;Gene: celf

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11

||

Db 9 PR 10

RESULT 21

B43669

hypothetical protein (rhdA 5' region) - Synechococcus sp. (fragment)

C;Species: Synechococcus sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C;Accession: B43669

R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.

J. Bacteriol. 173, 2751-2760, 1991

A;Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasmically localized protein with sequence similarity to rhodanese.

A;Reference number: A43669; MUID:91210163; PMID:1708376

A;Accession: B43669

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-11 <LAU>
A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 6 AK 7

RESULT 22

D60691

phycobilisome 9K linker protein - Synechococcus sp. (PCC 7002) (fragment)

C;Species: Synechococcus sp.

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999

C;Accession: D60691

R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.

Arch. Microbiol. 153, 550-560, 1990

A;Title: Structural and compositional analyses of the phycobilisomes of Synechococcus sp. PCC 7002. Analyses of the wild-type strain and a phycocyanin-less mutant constructed by interposon mutagenesis.

A;Reference number: A60691; MUID:90314662; PMID:2164365

A;Accession: D60691

A;Molecule type: protein

A;Residues: 1-11 <BRY>

C;Comment: This protein, one of the eleven components detected in this species of the phycobilisome that helps to trap light energy for photosystem II, does not carry a chromophore.

C;Keywords: photosystem II

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 3 SQ 4

RESULT 23

PC2372

58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus cereus.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-11 <MAS>
C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 1 AK 2

RESULT 24
E41476
probable antigen 5 - Mycobacterium leprae (fragment)
C;Species: Mycobacterium leprae
C;Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993
C;Accession: E41476
R;Hartskeerl, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.
Infect. Immun. 58, 2821-2827, 1990
A;Title: Selection and characterization of recombinant clones that produce Mycobacterium leprae antigens recognized by antibodies in sera from household contacts of leprosy patients.
A;Reference number: A41476; MUID:90354041; PMID:1696931
A;Accession: E41476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <HAR>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 2 SQ 3

RESULT 25
H54346
pyruvate synthase (EC 1.2.7.1) alpha chain - Pyrococcus furiosus (fragment)
C;Species: Pyrococcus furiosus
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-May-2000
C;Accession: H54346
R;Blamey, J.M.; Adams, M.W.
Biochemistry 33, 1000-1007, 1994
A;Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase from the hyperthermophilic bacterium, Thermotoga maritima.
A;Reference number: A54346; MUID:94137707; PMID:8305426
A;Accession: H54346
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BLA>
C;Keywords: coenzyme A; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 4 KG 5

RESULT 26

S70338

napin small chain S3A - Swedish turnip (fragment)
C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70338
R;Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 23-33, 1996
A;Title: Purification and sequencing of multiple forms of Brassica napus seed
napin small chains that are calmodulin antagonists and substrates for plant
calcium-dependent protein kinase.
A;Reference number: S70336; MUID:96283790; PMID:8679670
A;Accession: S70338
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <NEU>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 1 QA 2

RESULT 27

G61497

seed protein ws-23 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: G61497
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from
two-dimensional gel.
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: G61497
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HIR>
C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5

||
Db 1 AK 2

RESULT 28
S19775
wound-induced protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C;Accession: S19775
R;Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A;Reference number: S19773
A;Accession: S19775
A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 6 KG 7

RESULT 29
PU0029
33K protein 3218 - rice (strain Nohonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PU0029
R;Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A;Reference number: PS0208
A;Accession: PU0029
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: bran
C;Comment: molecular weight 33K, pI 6.0.

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 5 GP 6

RESULT 30
PS0259
39K protein 3225 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0259

R;Tsugita, A.; Kamo, M.
submitted to JIPID, April 1993
A;Reference number: PS0209
A;Accession: PS0259
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: callus
C;Comment: molecular weight 39K, pI 5.7.

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 6 GP 7

RESULT 31
S78026
ribosomal protein YmL29, mitochondrial - yeast (*Saccharomyces cerevisiae*)
(fragment)
C;Species: *Saccharomyces cerevisiae*
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C;Accession: S78026
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth,
E.; Wittmann-Liebold, B.; Nishimura, T.; Isono, K.
Eur. J. Biochem. 245, 449-456, 1997
A;Title: Identification and characterization of the genes for mitochondrial
ribosomal proteins of *Saccharomyces cerevisiae*.
A;Reference number: S78018; MUID:97296414; PMID:9151978
A;Accession: S78026
A;Molecule type: protein
A;Residues: 1-11 <KIT>
C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 8 PR 9

RESULT 32
A34135
DNA-binding protein p - *Crithidia fasciculata* mitochondrion (fragment)
C;Species: mitochondrion *Crithidia fasciculata*
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C;Accession: A34135
R;Tittawella, I.
FEBS Lett. 260, 57-61, 1990
A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan
Crithidia fasciculata.

A;Reference number: A34135
A;Accession: A34135
A;Molecule type: protein
A;Residues: 1-11 <TIT>
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 8 RK 9

RESULT 33

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)
N;Alternate names: phosphofructokinase; phosphohexokinase
C;Species: Ascaris suum (pig roundworm)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 28-Apr-1993
C;Accession: A26120
R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.
J. Biol. Chem. 262, 32-34, 1987
A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.
A;Reference number: A26120; MUID:87083467; PMID:3025208
A;Accession: A26120
A;Molecule type: protein
A;Residues: 1-11 <KUL>
C;Keywords: glycolysis; phototransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 1 AK 2

RESULT 34

B60769

Ig H2 chain - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C;Accession: B60769
R;Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A;Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A;Reference number: A60769; MUID:91060965; PMID:2123225
A;Accession: B60769
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-11 <HAN>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 1 SQ 2

RESULT 35

S33300

probable substance P - smaller spotted catshark

C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999

C;Accession: S33300

R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.

A;Reference number: S33300; MUID:93292508; PMID:7685693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAU>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 36

S43626

cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)

C;Species: Salmo sp. (trout)

C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998

C;Accession: S43626

R;Freund, R.; Kadenbach, B.

Eur. J. Biochem. 221, 1111-1116, 1994

A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.

A;Reference number: S43624; MUID:94237150; PMID:8181469

A;Accession: S43626

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <FRE>
C;Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory chain; transmembrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 4 KG 5

RESULT 37
C37196
bradykinin-potentiating peptide 3 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: C37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: C37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 3 GP 4

RESULT 38
D37196
bradykinin-potentiating peptide 4 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: D37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: D37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 3 GP 4

RESULT 39
E57789
gallbladder stone matrix protein, 25K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
C;Accession: E57789
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A;Description: The proteins of gallbladder stones.
A;Reference number: A57789
A;Accession: E57789
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 2 RK 3

RESULT 40
I54193
Rhesus blood group CcEe protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Accession: I54193
R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.;
Colin, Y.
Genomics 19, 68-74, 1994
A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe
antigens and characterization of the promoter region.
A;Reference number: I54193; MUID:94245182; PMID:8188244
A;Accession: I54193
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761
C;Genetics:
A;Gene: GDB:RHCE
A;Cross-references: GDB:229957; OMIM:111700
A;Map position: 1p36.2-1p34

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 10 RR 11

RESULT 41
D56979
collagen alpha 1(II) chain - bovine (fragment)
N;Alternate names: collagen alpha 3(XI) chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 11-Jul-1997
C;Accession: D56979
R;Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI
collagen. Insights on polymeric assembly.
A;Reference number: A56978; MUID:95370194; PMID:7642541
A;Accession: D56979
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <WUAA>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form 3(XI))
#status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 7 GP 8

RESULT 42
A14454
6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993
C;Accession: A14454
R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.
Biochem. Soc. Trans. 7, 721-723, 1979
A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.
A;Reference number: A14454; MUID:80004524; PMID:157899
A;Accession: A14454
A;Molecule type: protein
A;Residues: 1-11 <FOR>
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
 ||
Db 8 AK 9

RESULT 43

PH1632

Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1632
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1632
A;Molecule type: DNA
A;Residues: 1-11 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
 ||
Db 3 RR 4

RESULT 44

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1583
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1583
A;Molecule type: DNA
A;Residues: 1-11 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
 ||

Db 6 GP 7

RESULT 45
PH1375
T antigen variant K-2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: PH1375
R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product
select for transformed cells with point mutations within sequences encoding CTL
recognition epitopes.
A;Reference number: PH1373; MUID:92364547; PMID:1380062
A;Accession: PH1375
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 2 KG 3

RESULT 46
PH1376
T antigen variant K-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: PH1376
R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product
select for transformed cells with point mutations within sequences encoding CTL
recognition epitopes.
A;Reference number: PH1373; MUID:92364547; PMID:1380062
A;Accession: PH1376
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 2 KG 3

RESULT 47
PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0217
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0217
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 48
C38887
T-cell receptor gamma chain (5a.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C38887
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 1 AS 2

RESULT 49
I41946
T-cell receptor gamma chain (5t.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: I41946

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: I41946

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 1 AS 2

RESULT 50

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse
(fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.28%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5

||

Db 4 AK 5

RESULT 51

S53436

beta-D-galactosidase - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Aug-1995 #sequence_revision 15-May-1998 #text_change 07-May-1999

C;Accession: S53436; S53437

R;Tulsiani, D.R.P.; Skudlarek, M.D.; Araki, Y.; Orgebin-Crist, M.C.

Biochem. J. 305, 41-50, 1995

A;Title: Purification and characterization of two forms of beta-D-galactosidase from rat epididymal luminal fluid: evidence for their role in the modification of sperm plasma membrane glycoprotein(s).
A;Reference number: S53436; MUID:95126928; PMID:7826352
A;Accession: S53436
A;Molecule type: protein
A;Residues: 1-11 <TUL>
A;Experimental source: epididymal fluid
A;Note: 84K form
A;Accession: S53437
A;Molecule type: protein
A;Residues: 1-11 <TUW>
A;Experimental source: epididymal fluid
A;Note: 97K form
C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 5 SQ 6

RESULT 52
S65377
cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S65377
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65377
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <SCH>
C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 1 AS 2

RESULT 53
PH0939
T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0939
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0939
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 54
PH0940
T-cell receptor beta chain V-D-J region (clone 11) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0940
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0940
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 55
PH0941
T-cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0941
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0941
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 56

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0929

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandebark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0929

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 57

PH0891

T-cell receptor beta chain V-D-J region (clone 6-1) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0891

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandebark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0891

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 58

PH0938

T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0938

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandebark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0938

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 59

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandebark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from experimentally induced allergic encephalomyelitis

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 60

PH0903

T-cell receptor beta chain V-D-J region (hybridoma S1C2A6) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0903

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0903

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 61

PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0904

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0904

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 62
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 63
PH0919
T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0919
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0919
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon CAG for residue 11 as Glu
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 64
PH0914

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0914
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 65
PH0922
T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0922
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0922
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 66
PH0906
T-cell receptor beta chain V-D-J region (isolates 2, 8, 9) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0906
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0906

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 67

S60294

tubulin 2 beta-3 chain - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jun-2002

C;Accession: S60294

R;Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Bruhat, A.; Couderc, J.L.; Dastugue, B.

Insect Mol. Biol. 2, 39-48, 1993

A;Title: In *Drosophila Kc* cells 20-OHE induction of the 60C beta-3 tubulin gene expression is a primary transcriptional event.

A;Reference number: S60292; MUID:97242543; PMID:9087542

A;Accession: S60294

A;Molecule type: mRNA

A;Residues: 1-11 <CHA>

A;Cross-references: EMBL:X60393

C;Genetics:

A;Gene: FlyBase:beta-Tub60D

A;Cross-references: FlyBase:FBgn0003888

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2

||

Db 2 AS 3

RESULT 68

S19015

hypothetical protein 11 ruvC-yebC intergenic region - *Escherichia coli*

C;Species: *Escherichia coli*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: S19015

R;Sharples, G.J.; Lloyd, R.G.

J. Bacteriol. 173, 7711-7715, 1991

A;Title: Resolution of Holliday junctions in Escherichia coli: identification of the ruvC gene product as a 19-kilodalton protein.
A;Reference number: S19013; MUID:92041688; PMID:1657895
A;Accession: S19015
A;Molecule type: DNA
A;Residues: 1-11 <SHA>
A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174
C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 4 AK 5

RESULT 69
I54081
retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C;Accession: I54081
R;Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.;
Wang, Z.Y.; Larsen, C.J.; Berger, R.
Genes Chromosomes Cancer 6, 133-139, 1993
A;Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
primary structure of the reciprocal products of the PML-RARA gene in a patient
with t(15;17).
A;Reference number: I54081; MUID:93222087; PMID:7682097
A;Accession: I54081
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <DON>
A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588
A;Note: the translation is from an incorrect reading frame
C;Genetics:
A;Gene: GDB:RARA
A;Cross-references: GDB:120337; OMIM:180240
A;Map position: 17q12-17q12

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 10 KR 11

RESULT 70
ECLQ2M
tachykinin II - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08266
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990
A;Title: Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.
A;Reference number: S08265; MUID:90184489; PMID:2311766
A;Accession: S08266
A;Molecule type: protein
A;Residues: 1-11 <SCH>
C;Superfamily: tachykinin
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.18; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 71
SPHO
substance P - horse
C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.18; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 R 6
|
Db 1 R 1

RESULT 72
EOOCC
eledoisin - curled octopus
C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C;Accession: B01561; A01561
R;Anastasi, A.; Ersperer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.
A;Reference number: A01561
A;Accession: B01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 73
A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 R 6
|
Db 1 R 1

RESULT 74
EOOC
eledoisin - musky octopus
C;Species: Eledone moschata, Ozaena moschata (musky octopus)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998
C;Accession: A01561
R;Anastasi, A.; Erspamer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561
A;Accession: A01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 75
GMROL
leucosulfakinin - Madeira cockroach
N;Alternate names: LSK
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996
C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.
A;Reference number: A01622; MUID:86315858; PMID:3749893
A;Accession: A01622
A;Molecule type: protein
A;Residues: 1-11 <NAC>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 2 Q 2

Search completed: April 8, 2004, 15:49:27
Job time : 9.61538 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-15

Perfect score: 11

Sequence: 1 ASQAKRRKGPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published_Applications_AA:*

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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
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1	4	36.4	11	9	US-09-839-743-20	Sequence 20, Appl
2	4	36.4	11	10	US-09-726-470A-223	Sequence 223, App
3	4	36.4	11	14	US-10-301-357A-1	Sequence 1, Appli
4	3	27.3	11	8	US-08-801-405B-6	Sequence 6, Appli
5	3	27.3	11	9	US-09-073-009-30	Sequence 30, Appl
6	3	27.3	11	9	US-09-780-070-37	Sequence 37, Appl
7	3	27.3	11	9	US-09-815-108-9	Sequence 9, Appli
8	3	27.3	11	9	US-09-253-794-20	Sequence 20, Appl
9	3	27.3	11	9	US-09-056-160B-4	Sequence 4, Appli
10	3	27.3	11	9	US-09-030-619-20	Sequence 20, Appl
11	3	27.3	11	9	US-09-030-619-66	Sequence 66, Appl
12	3	27.3	11	9	US-09-030-619-101	Sequence 101, App
13	3	27.3	11	9	US-09-886-404-13	Sequence 13, Appl
14	3	27.3	11	9	US-09-805-805-8	Sequence 8, Appli
15	3	27.3	11	9	US-09-809-567-16	Sequence 16, Appl
16	3	27.3	11	9	US-09-802-109-1	Sequence 1, Appli
17	3	27.3	11	9	US-09-802-109-2	Sequence 2, Appli
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19	3	27.3	11	9	US-09-802-109-4	Sequence 4, Appli
20	3	27.3	11	9	US-09-802-109-5	Sequence 5, Appli
21	3	27.3	11	9	US-09-802-109-6	Sequence 6, Appli
22	3	27.3	11	9	US-09-802-109-7	Sequence 7, Appli
23	3	27.3	11	9	US-09-802-109-8	Sequence 8, Appli
24	3	27.3	11	9	US-09-821-821-24	Sequence 24, Appl
25	3	27.3	11	9	US-09-798-791-3	Sequence 3, Appli
26	3	27.3	11	9	US-09-192-854-6	Sequence 6, Appli
27	3	27.3	11	9	US-09-192-854-47	Sequence 47, Appl
28	3	27.3	11	9	US-09-192-854-51	Sequence 51, Appl
29	3	27.3	11	9	US-09-192-854-54	Sequence 54, Appl
30	3	27.3	11	9	US-09-192-854-56	Sequence 56, Appl
31	3	27.3	11	9	US-09-192-854-58	Sequence 58, Appl
32	3	27.3	11	9	US-09-192-854-83	Sequence 83, Appl
33	3	27.3	11	9	US-09-192-854-85	Sequence 85, Appl
34	3	27.3	11	9	US-09-192-854-110	Sequence 110, App
35	3	27.3	11	9	US-09-192-854-114	Sequence 114, App
36	3	27.3	11	9	US-09-192-854-122	Sequence 122, App
37	3	27.3	11	9	US-09-192-854-123	Sequence 123, App
38	3	27.3	11	9	US-09-192-854-134	Sequence 134, App
39	3	27.3	11	9	US-09-192-854-149	Sequence 149, App
40	3	27.3	11	9	US-09-192-854-153	Sequence 153, App
41	3	27.3	11	9	US-09-192-854-156	Sequence 156, App
42	3	27.3	11	9	US-09-192-854-163	Sequence 163, App
43	3	27.3	11	9	US-09-192-854-170	Sequence 170, App
44	3	27.3	11	9	US-09-192-854-177	Sequence 177, App
45	3	27.3	11	9	US-09-192-854-178	Sequence 178, App
46	3	27.3	11	9	US-09-192-854-179	Sequence 179, App
47	3	27.3	11	9	US-09-895-943-13	Sequence 13, Appl
48	3	27.3	11	9	US-09-780-662A-14	Sequence 14, Appl
49	3	27.3	11	9	US-09-023-588-30	Sequence 30, Appl
50	3	27.3	11	9	US-09-891-064A-6	Sequence 6, Appli
51	3	27.3	11	9	US-09-825-414-91	Sequence 91, Appl
52	3	27.3	11	9	US-09-861-294-6	Sequence 6, Appli
53	3	27.3	11	9	US-09-861-294-22	Sequence 22, Appl
54	3	27.3	11	9	US-09-793-306-30	Sequence 30, Appl
55	3	27.3	11	9	US-09-798-058-8	Sequence 8, Appli
56	3	27.3	11	9	US-09-867-274-23	Sequence 23, Appl

57	3	27.3	11	9	US-09-955-866-24	Sequence 24, Appl
58	3	27.3	11	9	US-09-976-165-54	Sequence 54, Appl
59	3	27.3	11	9	US-09-736-743A-2	Sequence 2, Appl
60	3	27.3	11	9	US-09-928-175-25	Sequence 25, Appl
61	3	27.3	11	9	US-09-995-542-13	Sequence 13, Appl
62	3	27.3	11	9	US-09-924-099-3	Sequence 3, Appl
63	3	27.3	11	9	US-09-872-832-29	Sequence 29, Appl
64	3	27.3	11	9	US-09-927-850-18	Sequence 18, Appl
65	3	27.3	11	9	US-09-974-449-46	Sequence 46, Appl
66	3	27.3	11	9	US-09-751-100B-4	Sequence 4, Appl
67	3	27.3	11	9	US-09-984-183-4	Sequence 4, Appl
68	3	27.3	11	9	US-09-828-708-37	Sequence 37, Appl
69	3	27.3	11	9	US-09-839-743-21	Sequence 21, Appl
70	3	27.3	11	9	US-09-839-743-24	Sequence 24, Appl
71	3	27.3	11	9	US-09-839-743-25	Sequence 25, Appl
72	3	27.3	11	9	US-09-949-196-15	Sequence 15, Appl
73	3	27.3	11	9	US-09-948-018-22	Sequence 22, Appl
74	3	27.3	11	9	US-09-949-559-4	Sequence 4, Appl
75	3	27.3	11	9	US-09-995-515-14	Sequence 14, Appl
76	3	27.3	11	9	US-09-895-593-13	Sequence 13, Appl
77	3	27.3	11	9	US-09-968-561A-10	Sequence 10, Appl
78	3	27.3	11	9	US-09-968-561A-16	Sequence 16, Appl
79	3	27.3	11	9	US-09-968-561A-22	Sequence 22, Appl
80	3	27.3	11	9	US-09-968-561A-28	Sequence 28, Appl
81	3	27.3	11	9	US-09-968-561A-34	Sequence 34, Appl
82	3	27.3	11	9	US-09-968-561A-40	Sequence 40, Appl
83	3	27.3	11	9	US-09-968-561A-46	Sequence 46, Appl
84	3	27.3	11	9	US-09-968-561A-52	Sequence 52, Appl
85	3	27.3	11	9	US-09-968-561A-64	Sequence 64, Appl
86	3	27.3	11	9	US-09-968-561A-70	Sequence 70, Appl
87	3	27.3	11	9	US-09-968-561A-76	Sequence 76, Appl
88	3	27.3	11	9	US-09-968-561A-82	Sequence 82, Appl
89	3	27.3	11	9	US-09-968-561A-88	Sequence 88, Appl
90	3	27.3	11	9	US-09-968-561A-94	Sequence 94, Appl
91	3	27.3	11	9	US-09-968-561A-100	Sequence 100, App
92	3	27.3	11	9	US-09-968-561A-106	Sequence 106, App
93	3	27.3	11	9	US-09-968-561A-112	Sequence 112, App
94	3	27.3	11	9	US-09-968-561A-118	Sequence 118, App
95	3	27.3	11	9	US-09-968-561A-124	Sequence 124, App
96	3	27.3	11	9	US-09-968-561A-130	Sequence 130, App
97	3	27.3	11	9	US-09-968-561A-136	Sequence 136, App
98	3	27.3	11	9	US-09-968-561A-142	Sequence 142, App
99	3	27.3	11	9	US-09-968-561A-148	Sequence 148, App
100	3	27.3	11	9	US-09-968-561A-154	Sequence 154, App

ALIGNMENTS

RESULT 1

US-09-839-743-20

; Sequence 20, Application US/09839743

; Patent No. US20020146824A1

; GENERAL INFORMATION:

; APPLICANT: The Salk Institute for Biological Sciences

; APPLICANT: Lamb, Christopher

; APPLICANT: Doerner, Peter

; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-20

Query Match 36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
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Db 2 AKRR 5

RESULT 2
US-09-726-470A-223
; Sequence 223, Application US/09726470A
; Publication No. US20030036628A1
; GENERAL INFORMATION:
; APPLICANT: Zheleva, Daniella I
; APPLICANT: Fischer, Peter M
; APPLICANT: McInnes, Campbell
; APPLICANT: Andrews, Martin JI
; APPLICANT: Chan, Weng C
; APPLICANT: Atkinson, Gail E
; TITLE OF INVENTION: p21 Peptides
; FILE REFERENCE: CCI-014
; CURRENT APPLICATION NUMBER: US/09/726,470A
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: GB 9928323.6
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 275
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 223
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pRb-derived
; OTHER INFORMATION: peptide
US-09-726-470A-223

Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKRR 7
Db 5 AKRR 8

RESULT 3
US-10-301-357A-1
; Sequence 1, Application US/10301357A
; Publication No. US20030187226A1
; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R.
; APPLICANT: Sleep, Darrell
; APPLICANT: Berezenko, Stephen
; APPLICANT: Woodrow, John R.
; APPLICANT: Johnson, Richard A.
; TITLE OF INVENTION: PROCESS OF HIGH PURITY ALBUMIN PRODUCTION
; FILE REFERENCE: CE0111D US
; CURRENT APPLICATION NUMBER: US/10/301,357A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/GB96/00449
; PRIOR FILING DATE: 1996-02-29
; PRIOR APPLICATION NUMBER: 378,859
; PRIOR FILING DATE: 1995-05-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-301-357A-1

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQA 4
Db 4 ASQA 7

RESULT 4
US-08-801-405B-6
; Sequence 6, Application US/08801405B
; Publication No. US20020019008A1
; GENERAL INFORMATION:
; APPLICANT: ROUGEOT, Catherine
; ROUGEON, Francois
; TITLE OF INVENTION: THERAPEUTIC USE OF THE SMR1 PROTEIN, THE
; SMR1 MATURATION PRODUCTS, SPECIFICALLY THE QHNPR
; PENTAPEPTIDE AS WELL AS ITS BIOLOGICALLY ACTIVE
; DERIVATIVES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,405B
; FILING DATE: 20-Feb-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 012880-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-801-405B-6

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
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Db 3 GPR 5

RESULT 5
US-09-073-009-30
; Sequence 30, Application US/09073009
; Patent No. US20010012888A1
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
TUBERCULOSIS AND METH
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Coumbia Center, 701 Fifth Ave.
; CITY: Seattle

; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,009
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.441C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis

US-09-073-009-30

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
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Db 4 ASQ 6

RESULT 6

US-09-780-070-37

; Sequence 37, Application US/09780070
; Patent No. US20020009752A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmater, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT DOMAINS
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-780-070-37

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 7

US-09-815-108-9

; Sequence 9, Application US/09815108
; Patent No. US20020009776A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815,108
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-815-108-9

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 8

US-09-253-794-20

; Sequence 20, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED

MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-253-794-20

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
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Db 2 ASQ 4

RESULT 9
US-09-056-160B-4
; Sequence 4, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.

; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-09-056-160B-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 10
US-09-030-619-20
; Sequence 20, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN
COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin Analogue
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: Xaa = Hydrophobic Residue
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: Xaa = Proline or Valine
; NAME/KEY: VARIANT
; LOCATION: (5)...(6)
; OTHER INFORMATION: Xaa = Hydrophobic Residue
; NAME/KEY: VARIANT
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa = Proline or Valine
; NAME/KEY: VARIANT
; LOCATION: (8)...(8)
; OTHER INFORMATION: Xaa = Hydrophobic Residue

US-09-030-619-20

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 9 RRK 11

RESULT 11

US-09-030-619-66

; Sequence 66, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN
COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B

; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-66

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 9 RRK 11

RESULT 12

US-09-030-619-101

; Sequence 101, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN
COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-101

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
|||
Db 9 RRK 11

RESULT 13
US-09-886-404-13
; Sequence 13, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide of HIV
; OTHER INFORMATION: TAT protein

US-09-886-404-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 5 KRR 7

RESULT 14
US-09-805-805-8
; Sequence 8, Application US/09805805
; Patent No. US20020037557A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B.
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-006-A1
; CURRENT APPLICATION NUMBER: US/09/805,805
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,786
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-805-805-8

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 15

US-09-809-567-16

; Sequence 16, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-09-809-567-16

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 16

US-09-802-109-1

; Sequence 1, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109

; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Cys not found in natural protein.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa is either Cys(biotin) or Lys(biotin) at this
; OTHER INFORMATION: position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Either Cys(biotin) or Lys(biotin) at this
; OTHER INFORMATION: position.
; OTHER INFORMATION: Peptide has an N-terminal carboxylic acid residue.
; OTHER INFORMATION: Peptide has a C-terminal amide group.

US-09-802-109-1

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 17

US-09-802-109-2

; Sequence 2, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: two extra Cys residues not found in the natural
; OTHER INFORMATION: protein.
; NAME/KEY: BINDING
; LOCATION: (10)

; OTHER INFORMATION: Cys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 18

US-09-802-109-3

; Sequence 3, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the
; OTHER INFORMATION: natural protein.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.

US-09-802-109-3

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 19

US-09-802-109-4

; Sequence 4, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:

; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: two extra Cys not found in the natural protein.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Cys is the D isomer at this position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Cys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 20
US-09-802-109-5
; Sequence 5, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the
; OTHER INFORMATION: natural protein.

; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Lys is D isomer at this position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-5

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 21

US-09-802-109-6

; Sequence 6, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 3, but with a substitution of
; OTHER INFORMATION: Arg to Gln.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Lys is the D isomer at this position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.

US-09-802-109-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 22

US-09-802-109-7

; Sequence 7, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
; OTHER INFORMATION: Gln to Pro.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.

US-09-802-109-7

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 23

US-09-802-109-8

; Sequence 8, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:
; OTHER INFORMATION: All amino acids in this sequence are D amino acid.
; NAME/KEY: BINDING
; LOCATION: (2)
; OTHER INFORMATION: D-Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-8

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 2 KRR 4

RESULT 24

US-09-821-821-24

; Sequence 24, Application US/09821821
; Patent No. US20020064823A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Calzone, Frank J.
; TITLE OF INVENTION: CD20/IgE-Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36938A
; CURRENT APPLICATION NUMBER: US/09/821,821
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 09/723,258
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 60/193,728
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-09-821-821-24

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 5 KRR 7

RESULT 25

US-09-798-791-3

; Sequence 3, Application US/09798791
; Patent No. US20020064850A1
; GENERAL INFORMATION:

; APPLICANT: HEYER, ARND G.
; APPLICANT: REHM, JOCHEN
; APPLICANT: WENDENBURG, REGINA
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES HAVING
; TITLE OF INVENTION: FRUCTOSYLTRANSFERASE ACTIVITY, AND THEIR USE
; FILE REFERENCE: MPG-9
; CURRENT APPLICATION NUMBER: US/09/798,791
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06319
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 198 40 028.4
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Aspergillus sydowi
US-09-798-791-3

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4
|||
Db 6 SQA 8

RESULT 26

US-09-192-854-6
; Sequence 6, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 27
US-09-192-854-47
; Sequence 47, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-47

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 28
US-09-192-854-51
; Sequence 51, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-51

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 29

US-09-192-854-54

; Sequence 54, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-54

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 30

US-09-192-854-56

; Sequence 56, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-56

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 31

US-09-192-854-58

; Sequence 58, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-58

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 32

US-09-192-854-83

; Sequence 83, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-83

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 33

US-09-192-854-85

; Sequence 85, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-85

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 34

US-09-192-854-110

; Sequence 110, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-110

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 35

US-09-192-854-114

; Sequence 114, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-114

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 36

US-09-192-854-122

; Sequence 122, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21

; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-122

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 37

US-09-192-854-123

; Sequence 123, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-123

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 38

US-09-192-854-134

; Sequence 134, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854

; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-134

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 39

US-09-192-854-149

; Sequence 149, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-149

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 40

US-09-192-854-153

; Sequence 153, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian

; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-153

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 41

US-09-192-854-156

; Sequence 156, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-156

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 42

US-09-192-854-163

; Sequence 163, Application US/09192854
; Patent No. US20020068276A1

; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-163

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 43

US-09-192-854-170

; Sequence 170, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-170

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 44

US-09-192-854-177
; Sequence 177, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-177

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 45

US-09-192-854-178
; Sequence 178, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-178

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 46
US-09-192-854-179
; Sequence 179, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-179

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 47
US-09-895-943-13
; Sequence 13, Application US/09895943
; Patent No. US20020068323A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-514-C
; CURRENT APPLICATION NUMBER: US/09/895,943
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,866
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-895-943-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 5 KRR 7

RESULT 48
US-09-780-662A-14
; Sequence 14, Application US/09780662A
; Patent No. US20020076741A1
; GENERAL INFORMATION:
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: Biosensor for Anthrax
; FILE REFERENCE: MBHB00-126-A
; CURRENT APPLICATION NUMBER: US/09/780,662A
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic peptide sequence
US-09-780-662A-14

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RRK 8
 |||
Db 1 RRK 3

RESULT 49
US-09-023-588-30
; Sequence 30, Application US/09023588
; Patent No. US20020081579A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark R.
; TITLE OF INVENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,588
; FILING DATE: 14-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-09-023-588-30

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 4 ASQ 6

RESULT 50
US-09-891-064A-6
; Sequence 6, Application US/09891064A
; Patent No. US20020082391A1
; GENERAL INFORMATION:
; APPLICANT: James M. Anderson
; APPLICANT: Christina M. Van Itallie
; TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug
; TITLE OF INVENTION: Absorption Using Occludin Inhibitors
; FILE REFERENCE: OCR-754.CIP
; CURRENT APPLICATION NUMBER: US/09/891,064A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 09/142,732
; PRIOR FILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: MS DOS
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; OTHER INFORMATION: construct used in experiments
US-09-891-064A-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 1 ASQ 3

RESULT 51

US-09-825-414-91

; Sequence 91, Application US/09825414
; Patent No. US20020083489A1
; GENERAL INFORMATION:
; APPLICANT: Collmer, Alan
; APPLICANT: Alfano, James R.
; APPLICANT: Charkowski, Amy O.
; TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
; TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
; FILE REFERENCE: 19603/3243
; CURRENT APPLICATION NUMBER: US/09/825,414
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,160
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/224,604
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/249,548
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: immunodeficiency virus TAT protein, transduction
; OTHER INFORMATION: domain

US-09-825-414-91

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 52

US-09-861-294-6

; Sequence 6, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 53

US-09-861-294-22

; Sequence 22, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-22

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 54
US-09-793-306-30
; Sequence 30, Application US/09793306
; Patent No. US20020098200A1
; GENERAL INFORMATION:
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Skeiky, Yasir
; APPLICANT: Ovendale, Pamela
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
; TITLE OF INVENTION: of Tuberculosis
; FILE REFERENCE: 014058-008740US
; CURRENT APPLICATION NUMBER: US/09/793,306
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/185,037
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/223,828
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: Tb465 ORF-1
US-09-793-306-30

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 4 ASQ 6

RESULT 55
US-09-798-058-8
; Sequence 8, Application US/09798058
; Patent No. US20020098523A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Wilton, Alison Jane
; APPLICANT: Smith, Stephen
; APPLICANT: Main, Sarah Helen
; TITLE OF INVENTION: Human antibodies against eotaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-058-8

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 56

US-09-867-274-23

; Sequence 23, Application US/09867274
; Patent No. US20020106650A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher
; APPLICANT: Gao, Yongming
; TITLE OF INVENTION: Cysteine Knot Polypeptides: Cloaked-2 Molecules and Uses Thereof
; FILE REFERENCE: 01017/37428
; CURRENT APPLICATION NUMBER: US/09/867,274
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/208,550
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/223,542
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV TAT peptide

US-09-867-274-23

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 57

US-09-955-866-24

; Sequence 24, Application US/09955866
; Patent No. US20020107363A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.

; APPLICANT: Holst, Paige
; APPLICANT: Yoshinaga, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00,759-A
; CURRENT APPLICATION NUMBER: US/09/955,866
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,867
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-955-866-24

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 58

US-09-976-165-54

; Sequence 54, Application US/09976165
; Patent No. US20020107383A1
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/976,165
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/565,538
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-976-165-54

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GPR 11
|||
Db 4 GPR 6

RESULT 59

US-09-736-743A-2

; Sequence 2, Application US/09736743A
; Patent No. US20020110869A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BRUDER, JOSEPH T
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING CHIMERIC PROTEIN AND RELATED VECTOR, CELL AND
; TITLE OF INVENTION: METHOD OF EXPRESSION
; FILE REFERENCE: 203591
; CURRENT APPLICATION NUMBER: US/09/736,743A
; CURRENT FILING DATE: 2000-12-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus

US-09-736-743A-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 60

US-09-928-175-25

; Sequence 25, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618A1ma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-928-175-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 61
US-09-995-542-13

; Sequence 13, Application US/09995542
; Patent No. US20020127647A1
; GENERAL INFORMATION:
; APPLICANT: Shutter, John
; APPLICANT: Ulias, Laarni
; TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-658-A
; CURRENT APPLICATION NUMBER: US/09/995,542
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,520
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-995-542-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 62
US-09-924-099-3

; Sequence 3, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099

; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-3

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 63
US-09-872-832-29
; Sequence 29, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE
THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-29

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AKR 6
|||
Db 5 AKR 7

RESULT 64
US-09-927-850-18
; Sequence 18, Application US/09927850
; Patent No. US20020137137A1

; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew
; APPLICANT: Wen, Duanzhi
; APPLICANT: Kelly, Michael
; TITLE OF INVENTION: Interferon-Like Molecules and Uses Thereof
; FILE REFERENCE: 99,372-F
; CURRENT APPLICATION NUMBER: US/09/927,850
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/724,860
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/169,720
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-927-850-18

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 5 KRR 7

RESULT 65
US-09-974-449-46

; Sequence 46, Application US/09974449
; Patent No. US20020141989A1
; GENERAL INFORMATION:
; APPLICANT: Kricek, Franz
; APPLICANT: Stadler, Beda
; APPLICANT: Vogel, Monique
; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
; TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E
TO
; TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR
; FILE REFERENCE: 4-30888A
; CURRENT APPLICATION NUMBER: US/09/974,449
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: PCT/EP00/03288
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-449-46

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 66
US-09-751-100B-4
; Sequence 4, Application US/09751100B
; Patent No. US20020142436A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mouse
US-09-751-100B-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GPR 11
 |||
Db 9 GPR 11

RESULT 67
US-09-984-183-4
; Sequence 4, Application US/09984183
; Patent No. US20020142983A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 042881/0130
; CURRENT APPLICATION NUMBER: US/09/984,183
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/457,354
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/111,973
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-984-183-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 68

US-09-828-708-37

; Sequence 37, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their participation in
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-828-708-37

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 69

US-09-839-743-21

; Sequence 21, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344

; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-21

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 3 KRR 5

RESULT 70

US-09-839-743-24

; Sequence 24, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-24

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 4 KRR 6

RESULT 71
US-09-839-743-25
; Sequence 25, Application US/09839743
; Patent No. US20020146824A1
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Lamb, Christopher
; APPLICANT: Doerner, Peter
; APPLICANT: Laible, Goetz
; TITLE OF INVENTION: No. US20020146824A1 Transcription Enhancer Element and
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
; FILE REFERENCE: SALKINS.008DV3
; CURRENT APPLICATION NUMBER: US/09/839,743
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/401,336
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 09/189,344
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/669,721
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-839-743-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 4 KRR 6

RESULT 72
US-09-949-196-15
; Sequence 15, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF
Cdc25A IN RESPONSE
; TITLE OF INVENTION: TO DNA DAMAGE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
US-09-949-196-15

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 73

US-09-948-018-22

; Sequence 22, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Peptide of HIV TAT protein

US-09-948-018-22

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
|||
Db 5 KRR 7

RESULT 74

US-09-949-559-4

; Sequence 4, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hTNF40 CDRL1
US-09-949-559-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
 |||
Db 2 ASQ 4

RESULT 75
US-09-995-515-14
; Sequence 14, Application US/09995515
; Patent No. US20020151695A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-659-A
; CURRENT APPLICATION NUMBER: US/09/995,515
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,476
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-995-515-14

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KRR 7
 |||
Db 5 KRR 7

Search completed: April 8, 2004, 16:35:47
Job time : 31.3077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-15

Perfect score: 11

Sequence: 1 ASQAKRRKGPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
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1	3	27.3	11	7	Q7YP62	Q7yp62 homo sapien
2	3	27.3	11	12	Q69269	Q69269 equine herp
3	2	18.2	11	2	Q8RKN1	Q8rkn1 escherichia
4	2	18.2	11	2	Q9R7U8	Q9r7u8 pseudomonas
5	2	18.2	11	2	Q9S623	Q9s623 prochloroco
6	2	18.2	11	2	Q9RQ60	Q9rq60 buchner ap
7	2	18.2	11	2	Q9EUZ3	Q9euz3 escherichia
8	2	18.2	11	2	Q8RMI8	Q8rmi8 enterococcu
9	2	18.2	11	2	P71228	P71228 escherichia
10	2	18.2	11	2	Q9K332	Q9k332 staphylococ
11	2	18.2	11	2	Q93MI7	Q93mi7 escherichia
12	2	18.2	11	2	P95518	P95518 pasteurella
13	2	18.2	11	2	Q47345	Q47345 escherichia
14	2	18.2	11	2	Q47420	Q47420 escherichia
15	2	18.2	11	2	Q56413	Q56413 escherichia
16	2	18.2	11	2	Q44237	Q44237 anabaena sp
17	2	18.2	11	2	Q9R446	Q9r446 neisseria g
18	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
19	2	18.2	11	2	Q47567	Q47567 escherichia
20	2	18.2	11	4	Q14759	Q14759 homo sapien
21	2	18.2	11	4	Q9Y3G2	Q9y3g2 homo sapien
22	2	18.2	11	4	O75811	O75811 homo sapien
23	2	18.2	11	4	Q15997	Q15997 homo sapien
24	2	18.2	11	4	Q9C057	Q9c057 homo sapien
25	2	18.2	11	4	Q9H3V7	Q9h3v7 homo sapien
26	2	18.2	11	4	Q8NI03	Q8ni03 homo sapien
27	2	18.2	11	4	Q9UE69	Q9ue69 homo sapien
28	2	18.2	11	4	Q9UH72	Q9uh72 homo sapien
29	2	18.2	11	4	Q16217	Q16217 homo sapien
30	2	18.2	11	5	Q26092	Q26092 pisaster oc
31	2	18.2	11	5	Q9NL65	Q9nl65 ascaris suu
32	2	18.2	11	5	Q9TWX6	Q9twx6 manduca sex
33	2	18.2	11	5	Q23876	Q23876 dictyosteli
34	2	18.2	11	5	Q9NFX0	Q9nfx0 drosophila
35	2	18.2	11	5	Q8MPQ3	Q8mpq3 caenorhabdi
36	2	18.2	11	5	P82699	P82699 leucophaea
37	2	18.2	11	5	P82700	P82700 leucophaea
38	2	18.2	11	6	Q9TTQ0	Q9ttq0 gorilla gor
39	2	18.2	11	6	Q9TRX2	Q9trx2 bos taurus
40	2	18.2	11	6	Q9TRX3	Q9trx3 bos taurus
41	2	18.2	11	7	O77880	O77880 oreochromis
42	2	18.2	11	7	O77907	O77907 oreochromis
43	2	18.2	11	7	O77897	O77897 oreochromis
44	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
45	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
46	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
47	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
48	2	18.2	11	8	Q8MER8	Q8mer8 dombeya til
49	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
50	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
51	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
52	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
53	2	18.2	11	8	Q8MERO	Q8mer0 hibiscus co
54	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
55	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi
56	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca
57	2	18.2	11	8	Q8SKP8	Q8skp8 ctenophorus

58	2	18.2	11	8	Q8MER7	Q8mer7 fioria viti
59	2	18.2	11	8	Q8HQX5	Q8hqx5 rhabdothamn
60	2	18.2	11	10	Q06626	Q06626 solanum tub
61	2	18.2	11	10	Q65901	Q65901 leavenworth
62	2	18.2	11	10	Q39784	Q39784 gossypium h
63	2	18.2	11	10	Q82070	Q82070 triticum ae
64	2	18.2	11	10	Q94IR5	Q94ir5 pinus radia
65	2	18.2	11	10	Q04131	Q04131 lycopersico
66	2	18.2	11	10	P83092	P83092 spinacia ol
67	2	18.2	11	11	Q9QXM6	Q9qxm6 mus musculu
68	2	18.2	11	11	Q99N81	Q99n81 mus musculu
69	2	18.2	11	11	Q60807	Q60807 mus musculu
70	2	18.2	11	11	Q9QYF6	Q9qyf6 mus musculu
71	2	18.2	11	11	Q62207	Q62207 mus musculu
72	2	18.2	11	11	Q8R2J7	Q8r2j7 mesocricetu
73	2	18.2	11	11	Q9QXN6	Q9qxn6 mus musculu
74	2	18.2	11	11	Q7TME3	Q7tme3 mus musculu
75	2	18.2	11	12	Q8JS92	Q8js92 hepatitis b
76	2	18.2	11	12	P89269	P89269 xestia c-ni
77	2	18.2	11	12	Q997C1	Q997c1 east africa
78	2	18.2	11	12	Q86565	Q86565 varicella-z
79	2	18.2	11	13	Q9PS64	Q9ps64 gallus gall
80	2	18.2	11	13	Q9PS22	Q9ps22 xenopus lae
81	2	18.2	11	13	Q800X7	Q800x7 chelydra se
82	2	18.2	11	13	Q7ZZI9	Q7zzi9 motacilla f
83	2	18.2	11	13	Q7ZZI6	Q7zzi6 motacilla f
84	2	18.2	11	13	Q7T285	Q7t285 geochelone
85	2	18.2	11	13	Q7T284	Q7t284 geochelone
86	2	18.2	11	13	Q7T283	Q7t283 geochelone
87	2	18.2	11	13	Q7SX72	Q7sx72 geochelone
88	2	18.2	11	13	Q7SX71	Q7sx71 geochelone
89	2	18.2	11	15	Q83410	Q83410 mouse mamma
90	2	18.2	11	15	Q9DYW4	Q9dyw4 human immun
91	1	9.1	11	2	Q9AIY6	Q9aiy6 carsonella
92	1	9.1	11	2	O68237	O68237 borrelia bu
93	1	9.1	11	2	Q9R790	Q9r790 borrelia ga
94	1	9.1	11	2	Q48933	Q48933 mycobacteri
95	1	9.1	11	2	Q47451	Q47451 escherichia
96	1	9.1	11	2	Q9AIZ7	Q9aiz7 carsonella
97	1	9.1	11	2	Q52526	Q52526 rhizobium s
98	1	9.1	11	2	Q8KHL0	Q8kh10 streptococc
99	1	9.1	11	2	Q9L4F7	Q9l4f7 bacillus ce
100	1	9.1	11	2	Q47602	Q47602 escherichia

ALIGNMENTS

RESULT 1

Q7YP62

ID Q7YP62 PRELIMINARY; PRT; 11 AA.
AC Q7YP62;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen (Fragment).
GN HLA-F.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RT "Partial genomic sequence of HLA-F gene.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY328516; AAP94210.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1208 MW; 2E0B6C5CC5AB45B8 CRC64;

Query Match 27.3%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQA 4
|||
Db 7 SQA 9

RESULT 2

Q69269
ID Q69269 PRELIMINARY; PRT; 11 AA.
AC Q69269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN IE.
OS Equine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kentucky A;
RX MEDLINE=90064773; PubMed=2555546;
RA Harty R.N., Colle C.F., Grundy F.J., O'Callaghan D.J.;
RT "Mapping the termini and intron of the spliced immediate-early
transcript of equine herpesvirus 1.";
RL J. Virol. 63:5101-5110(1989).
DR EMBL; M30497; AAA66553.1; -.
KW Hypothetical protein.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1224 MW; D93837E0CAB5A416 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASQ 3
|||
Db 2 ASQ 4

RESULT 3

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.

AC Q8RKN1;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Beta-lactamase CTX-M-9 (Fragment).

GN BLACTX-M-9.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=743-D;

RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,

RA Prats G.;

RT "A novel complex sul1-type integron in Escherichia coli carrying the

RT bla(CTX-M-9) gene.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY092058; AAM15718.1; -.

FT NON_TER 1 1

SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 1 AS 2

RESULT 4

Q9R7U8

ID Q9R7U8 PRELIMINARY; PRT; 11 AA.

AC Q9R7U8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE DNR protein (A regulatory protein for the expression of the NiR and

DE nor genes) (Fragment).

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PAO1;

RX MEDLINE=95226457; PubMed=7711073;

RA Arai H., Igarashi Y., Kodama T.;

RT "The structural genes for nitric oxide reductase from Pseudomonas

RT aeruginosa.";

RL Biochim. Biophys. Acta 1261:279-284(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=PAO1;
RX MEDLINE=95394152; PubMed=7664887;
RA Arai H., Igarashi Y., Kodama T.;
RT "Expression of the nir and nor genes for denitrification of
RT Pseudomonas aeruginosa requires a novel CRP/FNR-related
RT transcriptional regulator, DNR, in addition to ANR.";
RL FEBS Lett. 371:73-76(1995).
DR EMBL; D50019; BAA08746.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 7 RR 8

RESULT 5
Q9S623
ID Q9S623 PRELIMINARY; PRT; 11 AA.
AC Q9S623;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070168; AAD23221.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1153 MW; 5F551A5CB05866D3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 9 GP 10

RESULT 6
Q9RQ60
ID Q9RQ60 PRELIMINARY; PRT; 11 AA.
AC Q9RQ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Acetohydroxy acid synthase small subunit (Fragment).
GN ILVH.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF129503; AAF13796.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1330 MW; 0E89EF1E2045B050 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 2 KR 3

RESULT 7
Q9EUZ3
ID Q9EUZ3 PRELIMINARY; PRT; 11 AA.
AC Q9EUZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribosome binding factor A (Fragment).
GN RBFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IQ490;
RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
RA Mortensen K.K.;
RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
RT IQ490.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ132862; CAC20133.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AK 5
 ||
Db 2 AK 3

RESULT 8

Q8RMI8
ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
AC Q8RMI8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ErmB (Fragment).
GN ERMB.
OS Enterococcus hirae.
OG Plasmid pMKH1.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1354;
RN [1]
RP SEQUENCE FROM N.A.
RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
RT poultry origin."
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF493942; AAM18554.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RK 8
 ||
Db 10 RK 11

RESULT 9

P71228
ID P71228 PRELIMINARY; PRT; 11 AA.
AC P71228;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nitrate/nitrite sensor transmitter (Fragment).
GN NARQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=92374842; PubMed=1508040;
RA Chiang R.C., Cavicchioli R., Gunsalus R.P.;

RT "Identification and characterization of narQ, a second nitrate sensor
RT for nitrate-dependent gene regulation in Escherichia coli.";
RL Mol. Microbiol. 6:1913-1923(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=97113461; PubMed=8955321;
RA Cavicchioli R., Kolesnikow T., Chiang R.C., Gunsalus R.P.;
RT "Characterization of the aegA locus of Escherichia coli: control of
RT gene expression in response to anaerobiosis and nitrate.";
RL J. Bacteriol. 178:6968-6974(1996).
DR EMBL; L34011; AAB46943.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1200 MW; 52E1CFFCA2D77403 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 4 KR 5

RESULT 10
Q9K332
ID Q9K332 PRELIMINARY; PRT; 11 AA.
AC Q9K332;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Geh (Fragment).
GN GEH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=20187516; PubMed=10722640;
RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;
RT "Identification of a new repetitive element in Staphylococcus
RT aureus.";
RL Infect. Immun. 68:2344-2348(2000).
DR EMBL; AF195967; AAF60251.1; -.
DR EMBL; AF195963; AAF60243.1; -.
DR EMBL; AF195964; AAF60245.1; -.
DR EMBL; AF195965; AAF60247.1; -.
DR EMBL; AF195966; AAF60249.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4

||
Db 10 QA 11

RESULT 11
Q93MI7
ID Q93MI7 PRELIMINARY; PRT; 11 AA.
AC Q93MI7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adhesin (Fragment).
GN IHA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFT073;
RA Stell A.L.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF401752; AAK94916.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1203 MW; 8E2817ECBDD731B1 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 7 AS 8

RESULT 12
P95518
ID P95518 PRELIMINARY; PRT; 11 AA.
AC P95518;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein RpsA (Fragment).
GN RPSA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHL101;
RX MEDLINE=97164347; PubMed=9011038;
RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;
RT "Isolation and characterization of the integration host factor genes
of Pasteurella haemolytica.";
RL FEMS Microbiol. Lett. 146:181-188(1997).
DR EMBL; U56139; AAC44845.1; -.

FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDD6 CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 8 AK 9

RESULT 13

Q47345
ID Q47345 PRELIMINARY; PRT; 11 AA.
AC Q47345;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Leader peptide.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;
RT "Identification of two Escherichia coli K12 proteins which are induced
RT in response to pollutant stress.";
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 2-11 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=85134883; PubMed=6396419;
RA Hudson G.S., Davidson B.E.;
RT "Nucleotide sequence and transcription of the phenylalanine and
RT tyrosine operons of Escherichia coli K12.";
RL J. Mol. Biol. 180:1023-1051(1984).
DR EMBL; Z70523; CAA94435.1; -.
SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 10 KR 11

RESULT 14

Q47420
ID Q47420 PRELIMINARY; PRT; 11 AA.
AC Q47420;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF11 protein.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92041688; PubMed=1657895;
RA Sharples G.J., Lloyd R.G.;
RT "Resolution of Holliday junctions in Escherichia coli: Identification
of the ruvC gene product as a 19-Kilodalton protein.";
RL J. Bacteriol. 173:7711-7715(1991).
DR EMBL; X59551; CAA42127.1; -.
DR PIR; S19015; S19015.
SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 4 AK 5

RESULT 15

Q56413
ID Q56413 PRELIMINARY; PRT; 11 AA.
AC Q56413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IS602L region DNA, 5' end (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Transposon Tn602;
RX MEDLINE=87318208; PubMed=2819910;
RA Stibitz S., Davies J.E.;
RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";
RL Plasmid 17:202-209(1987).
DR EMBL; M22735; AAA27464.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||

Db 1 AK 2

RESULT 16

Q44237

ID Q44237 PRELIMINARY; PRT; 11 AA.
AC Q44237;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glutamine synthetase (Fragment).
GN GLNA.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;
RT "The apcF gene of Anabaena sp. strain PCC 7120 is regulated by
RT nitrogen and the apcF and glnA promoters overlap.";
RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Scappino L.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U21853; AAA65652.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6

||

Db 9 KR 10

RESULT 17

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.
AC Q9R446;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Carbamoyl-phosphate synthase subunit A (Fragment).
GN CARA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RX MEDLINE=95291461; PubMed=7773412;

RA Lawson F.S., Billowes F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF029363; AAC78453.1; -.
DR EMBL; AF029362; AAC78452.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 10 QA 11

RESULT 18
Q8GMU3
ID Q8GMU3 PRELIMINARY; PRT; 11 AA.
AC Q8GMU3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative catalase isozyme (Fragment).
GN KATA.
OS Acinetobacter lwoffii.
OG Plasmid pKLH202.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC108;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ250245; CAC80800.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
 ||
Db 2 SQ 3

RESULT 19

Q47567

ID Q47567 PRELIMINARY; PRT; 11 AA.
AC Q47567;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=94162733; PubMed=7764507;
RA Yamada M., Yanai S., Talkuder A.;
RT "Analysis of products of the Escherichia coli genomic genes and
regulation of their expressions: an applicable procedure for genomic
analysis of other microorganisms.";
RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
DR EMBL; D21154; BAA04690.1; -.
KW Hypothetical protein.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1272 MW; 3D66CACD07244DC7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GP 10
 ||
Db 3 GP 4

RESULT 20

Q14759

ID Q14759 PRELIMINARY; PRT; 11 AA.
AC Q14759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lymphocyte cytosolic protein 2 (Fragment).
GN LCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sunden S.L.F., Carr L.L., Clements J.L., Motto D.G., Koretzky G.A.;

RT "Polymorphism in and localization of the gene encoding the 76 kDa SH2
RT domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-
RT qter.";
RL Genomics 0:0-0(1995).
DR EMBL; U44065; AAA93308.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DDD CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 7 RK 8

RESULT 21
Q9Y3G2
ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.
AC Q9Y3G2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LSFR2 protein (Fragment).
GN LSFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299247; PubMed=10369878;
RA Gilley J., Fried M.;
RT "Extensive gene order differences within regions of conserved synteny
RT between the Fugu and human genomes: implications for chromosomal
RT evolution and the cloning of disease genes.";
RL Hum. Mol. Genet. 8:1313-1320(1999).
DR EMBL; Y17456; CAB44349.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 4 RK 5

RESULT 22
O75811
ID O75811 PRELIMINARY; PRT; 11 AA.
AC O75811;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ErbB-3 R2 (Fragment).
GN C-ERBB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=98345147; PubMed=9681822;
RA Lee H., Maihle N.J.;
RT "Isolation and characterization of four alternate c-erbB3 transcripts
RT expressed in ovarian carcinoma-derived cell lines and normal human
RT tissues.";
RL Oncogene 16:3243-3252(1998).
DR EMBL; U88358; AAC39858.1; --.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1017 MW; 21B236366EB72878 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 9 KG 10

RESULT 23
Q15997
ID Q15997 PRELIMINARY; PRT; 11 AA.
AC Q15997;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RARA protein (Fragment).
GN RARA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93222087; PubMed=7682097;
RA Dong S., Geng J.P., Tong J.H., Wu Y., Cai J.R., Sun G.L., Chen S.R.,
RA Wang Z.Y., Larsen C.J., Berger R., et al;
RT "Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
RT primary structure of the reciprocal products of the PML-RARA gene in a
RT patient with t(15;17).";
RL Genes Chromosomes Cancer 6:133-139(1993).
DR EMBL; S57794; AAD13888.1; --.
DR PIR; I54081; I54081.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 10 KR 11

RESULT 24

Q9C057
ID Q9C057 PRELIMINARY; PRT; 11 AA.
AC Q9C057;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEX (Fragment).
GN HEX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oyama Y., Kurabayashi M., Nagai R., Shimomura Y., Sekiguchi K.;
RT "Human Hex 5'-flanking sequence.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF182950; AAK12833.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1125 MW; 2644D7FE686761F7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 7 GP 8

RESULT 25

Q9H3V7
ID Q9H3V7 PRELIMINARY; PRT; 11 AA.
AC Q9H3V7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Aquaporin-4 (Fragment).
GN AQP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97008105; PubMed=8855281;

RA Lu M., Lee M.D., Smith B.L., Jung J.S., Agre P., Verdijk M.A.J.,
RA Merkx G., Rijss J.P.L., Deen P.M.T.;
RT "The human AQP4 gene: definition of the locus encoding two water
RT channel polypeptides in brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10908-10912(1996).
DR EMBL; U63613; AAG17964.1; -.
DR GO; GO:0005372; F:water transporter activity; NAS.
DR GO; GO:0006833; P:water transport; NAS.
KW Porin.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1233 MW; 379D9CA311AEB737 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 3 GP 4

RESULT 26
Q8NI03
ID Q8NI03 PRELIMINARY; PRT; 11 AA.
AC Q8NI03;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF500480; AAM21669.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 8 AS 9

RESULT 27
Q9UE69
ID Q9UE69 PRELIMINARY; PRT; 11 AA.
AC Q9UE69;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 5HT3 serotonin receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bedford F.K., Taylor S., Julius D., Ingraham H.A.;
RT "Expression of the 5HT3 serotonin receptor gene in neuronal cells is
regulated via novel NF-1 mediated complexes.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U73443; AAB71736.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1286 MW; 28F50414C6C6C2D3 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 7 QA 8

RESULT 28
Q9UH72
ID Q9UH72 PRELIMINARY; PRT; 11 AA.
AC Q9UH72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE V1-vascular vasopressin receptor AVPR1A (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thibonnier M., Willard H.F., Jeunemaitre X.;
RT "Study of V1-vascular vasopressin receptor gene microsatellite
polymorphisms in human essential hypertension.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF208541; AAF18470.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1071 MW; 8653B8E3B7687DC5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||

Db

6 GP 7

RESULT 29

Q16217

ID Q16217 PRELIMINARY; PRT; 11 AA.
AC Q16217;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Argininosuccinate synthetase protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95067972; PubMed=7977368;
RA Kobayashi K., Shaheen N., Terazono H., Saheki T.;
RT "Mutations in argininosuccinate synthetase mRNA of Japanese patients,
causing classical citrullinemia.";
RL Am. J. Hum. Genet. 55:1103-1112(1994).
DR EMBL; S73202; AAD14115.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1024 MW; 3DD920EC6B05B728 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 1 GP 2

RESULT 30

Q26092

ID Q26092 PRELIMINARY; PRT; 11 AA.
AC Q26092;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last séquence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sea STAR histone H2B gene 5'region (Fragment).
OS Pisaster ochraceus (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.
OX NCBI_TaxID=7612;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sperm;
RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
RT "Organization and Unusual Expression of Histone Genes in the Sea Star
Pisaster ochraceus.";
RL J. Mol. Evol. 25:29-36(1987).
DR EMBL; X05619; CAA29106.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 5 AS 6

RESULT 31

Q9NL65
ID Q9NL65 PRELIMINARY; PRT; 11 AA.
AC Q9NL65;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ASABF-delta (Fragment).
GN ASABF-DELTA.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato Y.;
RT "Ascaris suum asabf-delta gene, exon 2.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB029815; BAA89496.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1187 MW; 8BADD0CD1EAB5861 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 9 KR 10

RESULT 32

Q9TWX6
ID Q9TWX6 PRELIMINARY; PRT; 11 AA.
AC Q9TWX6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
(Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]

RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;
RA Touhara K., Prestwich G.D.;
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
binding protein.";
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 3 QA 4

RESULT 33
Q23876
ID Q23876 PRELIMINARY; PRT; 11 AA.
AC Q23876;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82260445; PubMed=6286214;
RA McKeown M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL; K02957; AAA33150.1; -.
DR EMBL; K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 7 QA 8

RESULT 34
Q9NFX0
ID Q9NFX0 PRELIMINARY; PRT; 11 AA.
AC Q9NFX0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial aconitase (Fragment).

GN ACON OR MAC OR CG9244.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephdroioidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA Lind M.I.;
RT "Charaterisation of two iron regulatory proteins and mitochondrial
aconitase in Drosophila melanogaster.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ252019; CAB93522.1; -.
DR FlyBase; FBgn0010100; Acon.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 9 QA 10

RESULT 35
Q8MPQ3
ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.
AC Q8MPQ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Y23H5A.8b.
GN Y23H5A.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Dempsey S., Le T.T.;
RT "The sequence of C. elegans cosmid Y23H5A.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF077541; AAM54173.1; -.
DR WormPep; Y23H5A.8b; CE31097.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 4 RR 5

RESULT 36
P82699
ID P82699 PRELIMINARY; PRT; 11 AA.
AC P82699;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-2 (LEM-PVK-2).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia, and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinins from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1102.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 2F4D9FFD85B05728 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 9 PR 10

RESULT 37

P82700

ID P82700 PRELIMINARY; PRT; 11 AA.
 AC P82700;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Periviscerokinin-3 (LEM-PVK-3).
 OS Leucophaea maderae (Madeira cockroach),
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Blaberus craniifer,
 OS Blaptica dubia (Argentinian wood cockroach), and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetz T., Schoofs L.;
 RT "Identification of novel periviscerokinins from single neurohaemal
 RT release sites in insects. MS/MS fragmentation complemented by Edman
 RT degradation.";
 RL Eur. J. Biochem. 267:3869-3873(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
 ||
 Db 9 PR 10

RESULT 38

Q9TTQ0

ID Q9TTQ0 PRELIMINARY; PRT; 11 AA.
 AC Q9TTQ0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Alanine glyoxylate aminotransferase (EC 2.6.1.44) (Fragment).
 GN AGT.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20188798; PubMed=10723739;
RA Holbrook J.D., Birdsey G.M., Yang Z., Bruford M.W., Danpure C.J.;
RT "Molecular adaptation of alanine Glyoxylate aminotransferase targeting
RT in primates.";
RL Mol. Biol. Evol. 17:387-400(2000).
DR EMBL; AJ237887; CAB56788.1; -.
DR GO; GO:0008453; F:alanine-glyoxylate transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Aminotransferase; Transferase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1193 MW; E9F82B8BC7272331 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 39
Q9TRX2
ID Q9TRX2 PRELIMINARY; PRT; 11 AA.
AC Q9TRX2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91308094; PubMed=1854724;
RA Ozturk D.H., Colman R.F.;
RT "Identification of cysteine-319 as the target amino acid of 8-[(4-
RT bromo-2,3-dioxobutyl)thio]adenosine 5'-triphosphate in bovine liver
RT glutamate dehydrogenase.";
RL Biochemistry 30:7126-7134(1991).
DR GO; GO:0004353; F:glutamate dehydrogenase [NAD(P)] activity; IEA.
SQ SEQUENCE 11 AA; 1207 MW; F46BF756A771B401 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 2 SQ 3

RESULT 40

Q9TRX3

ID Q9TRX3 PRELIMINARY; PRT; 11 AA.

AC Q9TRX3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=91308094; PubMed=1854724;

RA Ozturk D.H., Colman R.F.;

RT "Identification of cysteine-319 as the target amino acid of 8-[(4-bromo-2,3-dioxobutyl)thio]adenosine 5'-triphosphate in bovine liver glutamate dehydrogenase.";

RL Biochemistry 30:7126-7134(1991).

DR GO; GO:0004353; F:glutamate dehydrogenase [NAD(P)] activity; IEA.

SQ SEQUENCE 11 AA; 1292 MW; 9712A274B401F6C5 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
||
Db 4 SQ 5

RESULT 41

O77880

ID O77880 PRELIMINARY; PRT; 11 AA.

AC O77880;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 2 (Fragment).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;

OC Cichlidae; Oreochromis.

OX NCBI_TaxID=8128;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98315113; PubMed=9649539;

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

RA Figueroa F., Sultmann H., Klein J.;

RT "Linkage relationships and haplotype polymorphism among cichlid mhc class II B loci.";

RL Genetics 149:1527-1537(1998).

DR EMBL; AF049989; AAC41328.1; -.

FT NON_TER 1 1

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1346 MW; AB5F2D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 8 KR 9

RESULT 42
077907
ID 077907 PRELIMINARY; PRT; 11 AA.
AC 077907;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 2 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleoste;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050018; AAC41357.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1346 MW; AB5F2D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 8 KR 9

RESULT 43
077897
ID 077897 PRELIMINARY; PRT; 11 AA.
AC 077897;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050007; AAC41346.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1280 MW; BCD47D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 8 KR 9

RESULT 44
Q8MEL7
ID Q8MEL7 PRELIMINARY; PRT; 11 AA.
AC Q8MEL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Sida hookeriana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.
OX NCBI_TaxID=108446;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384624; AAM50396.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 45

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
AC Q8MEM2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Lagunaria patersonia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
OX NCBI_TaxID=183274;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384616; AAM50388.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 46

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
AC Q8MES5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Abelmoschus manihot.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
OX NCBI_TaxID=183220;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384561; AAM50399.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 47
Q8MEP0
ID Q8MEP0 PRELIMINARY; PRT; 11 AA.
AC Q8MEP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus peralbus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183256;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384598; AAM50370.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6

||
Db 1 KR 2

RESULT 48

Q8MER8

ID Q8MER8 PRELIMINARY; PRT; 11 AA.
AC Q8MER8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Dombeya tiliacea.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Dombeyoideae; Dombeya.
OX NCBI_TaxID=121875;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384569; AAM50407.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1424 MW; 7227C351D32AE9D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 49

Q8MES1

ID Q8MES1 PRELIMINARY; PRT; 11 AA.
AC Q8MES1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne pinoniana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183226;
RN [1]

RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384566; AAM50404.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 KR 6
 ||
 Db 1 KR 2

 RESULT 50
 Q8MEP3
 ID Q8MEP3 PRELIMINARY; PRT; 11 AA.
 AC Q8MEP3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus normanii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384595; AAM50367.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 KR 6
 ||
 Db 1 KR 2

RESULT 51

Q8MEQ7

ID Q8MEQ7 PRELIMINARY; PRT; 11 AA.
AC Q8MEQ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus drummondii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183239;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384581; AAM50353.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 52

Q8MEL9

ID Q8MEL9 PRELIMINARY; PRT; 11 AA.
AC Q8MEL9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Pavonia hastata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Pavonia.
OX NCBI_TaxID=183278;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using

RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384622; AAM50394.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 53
Q8MERO
ID Q8MERO PRELIMINARY; PRT; 11 AA.
AC Q8MERO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus coatesii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183236;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384578; AAM50416.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 54
Q8MES3

ID Q8MES3 PRELIMINARY; PRT; 11 AA.
 AC Q8MES3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Alyogyne cravenii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
 OX NCBI_TaxID=183223;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384563; AAM50401.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 KR 6
 ||
 Db 1 KR 2

RESULT 55
 Q8MEP5
 ID Q8MEP5 PRELIMINARY; PRT; 11 AA.
 AC Q8MEP5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus microchlaenus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183251;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384593; AAM50365.1; -

DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 56
Q8MER1
ID Q8MER1 PRELIMINARY; PRT; 11 AA.
AC Q8MER1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus calyphyllus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183235;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384577; AAM50415.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 57
Q8SKP8
ID Q8SKP8 PRELIMINARY; PRT; 11 AA.
AC Q8SKP8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Ctenophorus caudicinctus (Ring-tailed dragon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Ctenophorus.
OX NCBI_TaxID=180905;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21623804; PubMed=11754013;
RA Melville J., Schulte J.A. II, Larson A.;
RT "A molecular phylogenetic study of ecological diversification in the
RT Australian lizard genus Ctenophorus.";
RL J. Exp. Zool. 291:339-353(2001).
DR EMBL; AF375623; AAL78791.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1354 MW; A8F7371E33640336 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 5 KR 6

RESULT 58
Q8MER7
ID Q8MER7 PRELIMINARY; PRT; 11 AA.
AC Q8MER7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Fioria vitifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Fioria.
OX NCBI_TaxID=183231;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384570; AAM50408.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;
Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 1 KR 2

RESULT 59

Q8HQX5

ID Q8HQX5 PRELIMINARY; PRT; 11 AA.
AC Q8HQX5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose 1,5 bisphosphate carboxylase large subunit (EC 4.1.1.39)
DE (Fragment).
GN RBCL.
OS Rhabdothamnopsis sinensis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Rhabdothamnopsis.
OX NCBI_TaxID=199121;
RN [1]
RP SEQUENCE FROM N.A.
RA Mayer V.E., Moeller M., Perret M., Weber A.;
RT "Phylogenetic position and generic differentiation of Epithemateae
RT (Gesneriaceae) inferred from cpDNA sequence data.";
RL Am. J. Bot. 0:0-0(0).
DR EMBL; AJ490915; CAD36598.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
KW Lyase; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1178 MW; C2833DEA21AB01B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 9 AS 10

RESULT 60

Q06626

ID Q06626 PRELIMINARY; PRT; 11 AA.
AC Q06626;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Patatin A gene protein (Fragment).
GN PATATIN A GENE.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93081729; PubMed=1450383;
RA Nap J.P., Dirkse W.G., Louwerse J., Onstenk J., Visser R., Loonen A.,
RA Heidekamp F., Stiekema W.J.;
RT "Analysis of the region in between two closely linked patatin genes:
RT class II promoter activity in tuber, root and leaf.";
RL Plant Mol. Biol. 20:683-694(1992).
DR EMBL; S51460; AAB24400.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1301 MW; 95577379DB1B1451 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KR 6
||
Db 10 KR 11

RESULT 61
O65901
ID O65901 PRELIMINARY; PRT; 11 AA.
AC O65901;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoglucose isomerase (Fragment).
GN PGIC.
OS Leavenworthia crassa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Leavenworthia.
OX NCBI_TaxID=70805;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. CR8919/CR15, and cv. CR8919/CD6;
RA Liu F., Charlesworth D., Kreitman M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF054493; AAC19033.1; -.
DR EMBL; AF054492; AAC19032.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1208 MW; 5026B3A4BDD87337 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 7 AS 8

RESULT 62

Q39784

ID Q39784 PRELIMINARY; PRT; 11 AA.
AC Q39784;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE Alcohol dehydrogenase 2b-2 (Fragment).
OS *Gossypium hirsutum* (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; *Gossypium*.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Blue Tag Siokra;
RA Millar A.A., Dennis E.S.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U53705; AAA98988.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1161 MW; D67F443942D6D87D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 10 AK 11

RESULT 63

O82070

ID O82070 PRELIMINARY; PRT; 11 AA.
AC O82070;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RNA polymerase (EC 2.7.7.6) (Fragment).
OS *Triticum aestivum* (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; *Triticum*.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;

RT "Characterization of a gene encoding a single-subunit RNA polymerase from maize which is alternatively spliced.";
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ005344; CAA06489.1; -.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.
DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.
DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Nucleotidyltransferase; Transferase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 6 RK 7

RESULT 64
Q94IR5
ID Q94IR5 PRELIMINARY; PRT; 11 AA.
AC Q94IR5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nonspecific lipid transfer protein (Fragment).
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRLTP9-ii58055;
RA Jones D.F.;
RT "Genetic mapping of the lipid transfer protein gene family in Pinus
RT radiata and Pinus taeda.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY029028; AAK40266.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; 471B518D473AE727 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 9 SQ 10

RESULT 65
Q04131

ID Q04131 PRELIMINARY; PRT; 11 AA.
AC Q04131;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wound induced protein (Fragment).
OS *Lycopersicon esculentum* (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pik-red; TISSUE=Pericarp;
RX MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit:
RT interactions with fruit development, ethylene and light.";
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL; X59884; CAA42539.1; -.
DR PIR; S19775; S19775.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 6 KG 7

RESULT 66
P83092
ID P83092 PRELIMINARY; PRT; 11 AA.
AC P83092;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 33.6 kDa protein (Fragment).
OS *Spinacia oleracea* (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;
RL Submitted (AUG-2001) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 95344C4D21AAB775 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 10 PR 11

RESULT 67

Q9QXM6

ID Q9QXM6 PRELIMINARY; PRT; 11 AA.
AC Q9QXM6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamate receptor A (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bass B.L., Aruscavage P.J.;
RT "A phylogenetic analysis reveals an unusual sequence conservation
within introns involved in RNA editing."
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF201342; AAF23954.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1077 MW; C85710C5732771AD CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 7 KG 8

RESULT 68

Q99N81

ID Q99N81 PRELIMINARY; PRT; 11 AA.
AC Q99N81;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Delta like 1 (Fragment).
GN DLL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Nakayama K.;
RT "Multiple POU-binding motifs, recognized by tissue-specific nuclear
RT factor(S), are important for Dll1 gene expression in developing neural
RT precursor cells.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB050457; BAB43867.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1259 MW; 33C3634CBDC40B07 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 7 AS 8

RESULT 69
Q60807
ID Q60807 PRELIMINARY; PRT; 11 AA.
AC Q60807;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Medium-chain acyl-CoA dehydrogenase (Fragment).
GN ACADM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR-Swiss;
RA Tolwani R.J., Farmer S.C., Johnson K.R., Davisson M.T., Kurtz D.M.,
RA Hinsdale M.E., Cresci S., Kelly D.P., Wood P.A.;
RT "Gene-Promoter Structure and Chromosomal Location of the Mouse Medium-
RT Chain Acyl-CoA Dehydrogenase Gene.";
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U21488; AAA83256.1; -.
DR MGD; MGI:87867; Acadm.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1223 MW; 39815481641409C8 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 6 RR 7

RESULT 70
Q9QYF6
ID Q9QYF6 PRELIMINARY; PRT; 11 AA.
AC Q9QYF6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Pancreas transcription factor1 p48 subunit (Fragment).
GN PTF1P48.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129sv;
RA Obata J., Mimura H., Goto T., Nakayama R., Kondo M., Oka C.,
RA Kawaichi M.;
RT "p48 subunit of mouse PTF1 binds to RBP-Jkappa/CBF-1, the
RT intracellular mediator of Notch signaling, and is expressed in the
RT neural tube of the early stage embryos.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB035674; BAA88247.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1327 MW; CA4662F8E3372732 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 10 PR 11

RESULT 71
Q62207
ID Q62207 PRELIMINARY; PRT; 11 AA.
AC Q62207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Schwannomin (Fragment).
GN NF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95072570; PubMed=7981675;
RA Huynh D.P., Nechiporuk T., Pulst S.-M.;
RT "Alternative transcripts in the mouse neurofibromatosis type 2 (NF2)
RT gene are conserved and code for schwannomins with distinct C-terminal
RT domains.";
RL Hum. Mol. Genet. 3:1075-1079(1994).
DR EMBL; L28838; AAA57151.1; -.
DR PIR; I54368; I54368.
DR MGD; MGI:97307; Nf2.
FT NON_TER 1 1

SQ SEQUENCE 11 AA; 1238 MW; C51FA05774140866 CRC64;
Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 2 QA 3

RESULT 72

Q8R2J7

ID Q8R2J7 PRELIMINARY; PRT; 11 AA.
AC Q8R2J7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Microphthalmia-associated transcription factor (Fragment).
GN MITF.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Graw J., Pretsch W., Loester I.;
RT "Mutation in intron 6 of the hamster mitf gene leads to skipping of
the subsequent exon and creates a dominant animal model for the human
Waardenburg syndrome type II.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ458439; CAD30263.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1532 MW; 69D76B515449D414 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 2 RR 3

RESULT 73

Q9QXN6

ID Q9QXN6 PRELIMINARY; PRT; 11 AA.
AC Q9QXN6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-2 (Fragment).
GN IL2.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=20243845; PubMed=10779485;
 RA Lyons P.A., Armitage N., Argentina F., Denny P., Hill N.J., Lord C.J.,
 RA Wilusz M.B., Peterson L.B., Wicker L.S., Todd J.A.;
 RT "Congenic mapping of the type 1 diabetes locus, idd3, to a 780-kb
 RT region of mouse chromosome 3: identification of a candidate segment of
 RT ancestral DNA by haplotype mapping.";
 RL Genome Res. 10:446-453(2000).
 DR EMBL; AF195955; AAF22748.1; -.
 DR MGD; MGI:96548; Il12.
 DR GO; GO:0008283; P:cell proliferation; IMP.
 DR GO; GO:0006952; P:defense response; IMP.
 DR GO; GO:0006954; P:inflammatory response; IMP.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1233 MW; AE23EC9CBDD736D6 CRC64;

 Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AS 2
 ||
 Db 7 AS 8

RESULT 74
 Q7TME3
 ID Q7TME3 PRELIMINARY; PRT; 11 AA.
 AC Q7TME3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE UORF2 (UORF).
 GN EIF5A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jenkins Z.A., Johansson H.E.;
 RT "Mouse eIF5A, genes and mRNAs.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY129323; AAN17520.1; -.
 DR EMBL; AY129327; AAN17533.1; -.
 SQ SEQUENCE 11 AA; 1223 MW; 0685D1295862C73B CRC64;

 Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 10 AS 11

RESULT 75

Q8JS92

ID Q8JS92 PRELIMINARY; PRT; 11 AA.
AC Q8JS92;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE X protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=34;
RX PubMed=12185284;
RA Hou J., Lin Y., Waters J., Wang Z., Min J., Liao H., Jiang J.,
RA Chen J., Luo K., Karayiannis P.;
RT "Detection and significance of a G1862T variant of hepatitis B virus
RT in Chinese patients with fulminant hepatitis.";
RL J. Gen. Virol. 83:2291-2298(2002).
DR EMBL; AF495695; AAM34089.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1315 MW; DC70528AB5B73412 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 9 RR 10

Search completed: April 8, 2004, 15:46:07
Job time : 27.7692 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
(without alignments)
111.135 Million cell updates/sec

Title: US-09-787-443A-15

Perfect score: 11

Sequence: 1 ASQAKRRKGPR 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2	18.2	11	1	BPP3_BOTIN	P30423 bothrops in
2	2	18.2	11	1	BPP4_BOTIN	P30424 bothrops in
3	2	18.2	11	1	BPPB_AGKHA	P01021 agkistrodon
4	2	18.2	11	1	BPP_AGKHP	P04562 agkistrodon
5	2	18.2	11	1	BRK_MEGFL	P12797 megascolia
6	2	18.2	11	1	NXSN_PSETE	P59072 pseudonaja
7	2	18.2	11	1	OAIF_SARBU	P83518 sarcophaga
8	2	18.2	11	1	PKC1_CARMO	P82684 carausius m
9	2	18.2	11	1	PVK1_PERAM	P41837 periplaneta
10	2	18.2	11	1	Q2OA_COMTE	P80464 comamonas t
11	2	18.2	11	1	RR2_CONAM	P42341 conopholis
12	2	18.2	11	1	TIN1_HOPTI	P82651 hoplobatrac
13	2	18.2	11	1	TKN1_UPEIN	P82026 uperoleia i
14	2	18.2	11	1	TKN2_UPERU	P08616 uperoleia r
15	2	18.2	11	1	TKNA_CHICK	P19850 gallus gall
16	2	18.2	11	1	TKNA_GADMO	P28498 gadus morhu
17	2	18.2	11	1	TKNA_ONCMY	P28499 oncorhynchus

18	2	18.2	11	1	TKNA_SCYCA	P41333 scyliorhinu
19	2	18.2	11	1	TKN_PHYFU	P08615 physalaemus
20	2	18.2	11	1	UXB2_YEAST	P99013 saccharomyc
21	1	9.1	11	1	ANGT_CRIGE	P09037 crinia geor
22	1	9.1	11	1	ASL1_BACSE	P83146 bacteroides
23	1	9.1	11	1	ASL2_BACSE	P83147 bacteroides
24	1	9.1	11	1	CA21_LITCI	P82087 litoria cit
25	1	9.1	11	1	CA22_LITCI	P82088 litoria cit
26	1	9.1	11	1	CA31_LITCI	P82089 litoria cit
27	1	9.1	11	1	CA32_LITCI	P82090 litoria cit
28	1	9.1	11	1	CA41_LITCI	P82091 litoria cit
29	1	9.1	11	1	CA42_LITCI	P82092 litoria cit
30	1	9.1	11	1	CEP1_ACHFU	P22790 achatina fu
31	1	9.1	11	1	CORZ_PERAM	P11496 periplaneta
32	1	9.1	11	1	COXA_CANFA	P99501 canis famil
33	1	9.1	11	1	CSI5_BACSU	P81095 bacillus su
34	1	9.1	11	1	CX5A_CONAL	P58848 conus aulic
35	1	9.1	11	1	CX5B_CONAL	P58849 conus aulic
36	1	9.1	11	1	CXL1_CONMR	P58807 conus marmo
37	1	9.1	11	1	EFG_CLOPA	P81350 clostridium
38	1	9.1	11	1	ES1_RAT	P56571 rattus norv
39	1	9.1	11	1	FAR6_PENMO	P83321 penaeus mon
40	1	9.1	11	1	FAR9_CALVO	P41864 calliphora
41	1	9.1	11	1	HS70_PINPS	P81672 pinus pinas
42	1	9.1	11	1	LADD_ONCMY	P81018 oncorhynchu
43	1	9.1	11	1	LPW_THETH	P05624 thermus the
44	1	9.1	11	1	LSK1_LEUMA	P04428 leucophaea
45	1	9.1	11	1	LSKP_PERAM	P36885 periplaneta
46	1	9.1	11	1	MHBI_KLEPN	P80580 klebsiella
47	1	9.1	11	1	MLG_THETS	P41989 theromyzon
48	1	9.1	11	1	MORN_HUMAN	P01163 homo sapien
49	1	9.1	11	1	NUHM_CANFA	P49820 canis famil
50	1	9.1	11	1	PQQC_PSEFL	P55173 pseudomonas
51	1	9.1	11	1	RANC_RANPI	P08951 rana pipien
52	1	9.1	11	1	RE41_LITRU	P82074 litoria rub
53	1	9.1	11	1	RRPL_CHAV	P13179 chandipura
54	1	9.1	11	1	RS30_ONCMY	P83328 oncorhynchu
55	1	9.1	11	1	T2P1_PROVU	P31031 proteus vul
56	1	9.1	11	1	TIN4_HOPTI	P82654 hoplobatrac
57	1	9.1	11	1	TKC2_CALVO	P41518 calliphora
58	1	9.1	11	1	TKN1_PSEGU	P42986 pseudophryne
59	1	9.1	11	1	TKN1_UPERU	P08612 uperoleia r
60	1	9.1	11	1	TKN2_PSEGU	P42987 pseudophryne
61	1	9.1	11	1	TKN3_PSEGU	P42988 pseudophryne
62	1	9.1	11	1	TKN4_PSEGU	P42989 pseudophryne
63	1	9.1	11	1	TKN5_PSEGU	P42990 pseudophryne
64	1	9.1	11	1	TKNA_HORSE	P01290 equus cabal
65	1	9.1	11	1	TKNA_RANCA	P22688 rana catesbe
66	1	9.1	11	1	TKNA_RANRI	P29207 rana ridibu
67	1	9.1	11	1	TKND_RANCA	P22691 rana catesbe
68	1	9.1	11	1	TKN_ELEMO	P01293 eledone mos
69	1	9.1	11	1	UF05_MOUSE	P38643 mus musculu
70	1	9.1	11	1	ULAG_HUMAN	P31933 homo sapien

ALIGNMENTS

RESULT 1

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.

AC P30423;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI_TaxID=8723;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

DR PIR; C37196; C37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 3 GP 4

RESULT 2

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.

AC P30424;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI_TaxID=8723;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 angiotensin-converting enzyme and enhances the action of
 bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; D37196; D37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 9 GP 10
 ||
 Db 3 GP 4

RESULT 3
 BPPB_AGKHA
 ID BPPB_AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=242054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii.";
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 angiotensin-converting enzyme and enhances the action of
 bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 5 PR 6

RESULT 4
BPP_AGKHP
ID BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GP 10
||
Db 6 GP 7

RESULT 5
BRK_MEGFL
ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scoliidae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp Megascolia flavifrons.";
 RL Toxicon 25:527-535(1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascolia flavifrons.";
 RL Toxicon 26:34-34(1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . . ; TAS.
 KW Bradykinin; Vasodilator.
 FT PEPTIDE 1 11 MEGASCOLIAKININ.
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 9 RK 10

RESULT 6
 NXSN_PSETE
 ID NXSN_PSETE STANDARD; PRT; 11 AA.
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;

RA Gong N.L., Armugam A., Jeyaseelan K.;
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
RT cloning, expression and protein characterization.";
RL Eur. J. Biochem. 265:982-989(1999).
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
CC acetylcholine receptors (nAChR).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
CC -!- SIMILARITY: Belongs to the snake toxin family.
DR InterPro; IPR003571; Snake_toxin.
DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT UNSURE 3 3
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KG 9
||
Db 5 KG 6

RESULT 7
OAIF_SARBU
ID OAIF_SARBU STANDARD; PRT; 11 AA.
AC P83518;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
DE ODAIF(1-9); Neb-ODAIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=22272747; PubMed=12383874;
RA Vandingen A., Hens K., Baggerman G., Macours N., Schoofs L.,
RA De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme
RT substrate from vitellogenic ovaries of Neobellieria bullata.";
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
CC vitro.
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
CC terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.

FT PEPTIDE 1 11 NEB-ODAIF.
FT PEPTIDE 1 9 NEB-ODAIF(1-9).
FT PEPTIDE 1 7 NEB-ODAIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3
||
Db 6 SQ 7

RESULT 8

PKC1_CARMO
ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Prede R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
insect, Carausius morosus (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
activity).
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 9 PR 10

RESULT 9

PVK1_PERAM
ID PVK1_PERAM STANDARD; PRT; 11 AA.
AC P41837;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisynthetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
perisynthetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AS 2
||
Db 2 AS 3

RESULT 10
Q2OA_COMTE
ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: Converts (3-methyl)-quinoline to (3-methyl)-2-oxo-
CC 1,2-dihydroquinoline.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H₂O = isoquinolin-
CC 1(2H)-one + reduced acceptor.

CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
CC two gamma chains (Probable).
DR PIR; S66606; S66606.
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AK 5
||
Db 1 AK 2

RESULT 11
RR2_CONAM
ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S2 (Fragment).
GN RPS2.
OS Conopholis americana (Squawroot).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
of photosynthesis in a lineage of parasitic plants.";
RL Curr. Genet. 20:515-518(1991).
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.

KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RR 7
||
Db 3 RR 4

RESULT 12
TIN1_HOPTI
ID TIN1_HOPTI STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tigerinin-1.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 8 PR 9

RESULT 13
TKN1_UPEIN
ID TKN1_UPEIN STANDARD; PRT; 11 AA.

AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 QA 4
 ||
 Db 1 QA 2

RESULT 14
 TKN2_UPERU
 ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;

RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and bombesin-like peptides in the skin of the
RT Australian leptodactylid frog *Uperoleia rugosa*.";
RL Chem. Pharm. Bull. 28:689-695(1980).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 1 QA 2

RESULT 15
TKNA_CHICK
ID TKNA_CHICK STANDARD; PRT; 11 AA.
AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; JN0023; JN0023.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 16
TKNA_GADMO
ID TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23306; S23306.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 17

TKNA_ONCMY

ID TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neuropeptide-A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23308; S23308.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 18

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.

AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, *Scyliorhinus canicula*.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PR 11
||
Db 2 PR 3

RESULT 19
TKN_PHYFU
ID TKN_PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Leptodactylinae; Physalaemus.
OX NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=66076612; PubMed=5857249;

RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
RT "Structure and pharmacological actions of physalaemin, the main
RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
RL Experientia 20:489-490(1964).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07201; S07201.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QA 4
||
Db 1 QA 2

RESULT 20
UXB2_YEAST
ID UXB2_YEAST STANDARD; PRT; 11 AA.
AC P99013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RC STRAIN=X2180-1A;
RA Sanchez J.-C., Golaz O., Schaller D., Morsch F., Frutiger S.,
RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
RL Submitted (AUG-1995) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.20, its MW is: 9.2 kDa.
DR SWISS-2DPAGE; P99013; YEAST.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	7	RK	8
	11		
Db	8	RK	9

RESULT 21

ANGT CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80024575; PubMed=488254;
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endecapeptide from the skin of the Australian
RT frog Crinia georgiana.";
RL Experientia 35:1132-1133(1979).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S07207; S07207.
KW Vasoconstrictor.
SO SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

$$\begin{array}{rcc} Qy & 1 & A & 1 \\ & | \\ Db & 1 & A & 1 \end{array}$$

RESULT 22

ASL1 BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
AC P83146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.

RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 5 S 5

RESULT 23
ASL2_BACSE
ID ASL2_BACSE STANDARD; PRT; 11 AA.
AC P83147;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is

CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
|
Db 4 A 4

RESULT 24
CA21_LITCI
ID CA21_LITCI STANDARD; PRT; 11 AA.
AC P82087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 2.1/2.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 25
CA22_LITCI
ID CA22_LITCI STANDARD; PRT; 11 AA.
AC P82088;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 2.2/2.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!-- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!-- SUBCELLULAR LOCATION: Secreted.
CC -!-- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!-- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
CC sulfated.
CC -!-- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 26
CA31_LITCI
ID CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 Q 3
 |
 Db 1 Q 1

RESULT 27
 CA32_LITCI
 ID CA32_LITCI STANDARD; PRT; 11 AA.
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3 Q 3
Db	1 Q 1

RESULT 28
 CA41_LITCI
 ID CA41_LITCI STANDARD; PRT; 11 AA.
 AC P82091;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.1/4.1Y4.
 OS *Litoria citropa* (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.

CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 Q 3
 |
 Db 1 Q 1

RESULT 29
 CA42_LITCI
 ID CA42_LITCI STANDARD; PRT; 11 AA.
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 30
CEP1_ACHFU
ID CEP1_ACHFU STANDARD PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
CC excitatory actions on the penis retractor muscle, the buccal
CC muscle and the identified neurons controlling the buccal muscle
CC movement of achatina.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 1 S 1

RESULT 31
CORZ_PERAM
ID CORZ_PERAM STANDARD PRT; 11 AA.
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from
the American cockroach.";
RL FEBS Lett. 250:231-234(1989).
CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
in the physiological regulation of the heart beat.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; S05002; S05002.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 32
COXA_CANFA
ID COXA_CANFA STANDARD; PRT; 11 AA.
AC P99501;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
GN COX5A.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O₂ = 4 ferricyanochrome

CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
DR HSC-2DPAGE; P99501; DOG.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 1 S 1

RESULT 33
CSI5_BACSU
ID CSI5_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 R 6
|
Db 2 R 2

RESULT 34

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.

AC P58848;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Conotoxin au5a.

OS Conus aulicus (Court cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=89437;

RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=Venom;

RX MEDLINE=99452958; PubMed=10521453;

RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,

RA Bandyopadhyay P., Craig A.G., Olivera B.M.;

RT "The T-superfamily of conotoxins.";

RL J. Biol. Chem. 274:30664-30671(1999).

RN [2]

RP ERRATUM.

RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,

RA Bandyopadhyay P., Craig A.G., Olivera B.M.;

RL J. Biol. Chem. 274:36030-36030(1999).

CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is observed when injected into mice.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.

CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.

DR PIR; A59146; A59146.

KW Toxin.

FT DISULFID 2 9

FT DISULFID 3 10

SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 4 P 4

RESULT 35

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.

AC P58849;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Conotoxin au5b.

OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; B59146; B59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 4 P 4

RESULT 36
CXL1_CONMR
ID CXL1_CONMR STANDARD; PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;

RX MEDLINE=20564325; PubMed=10988292;
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RT venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522(2000).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11.
FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 G 9
|
Db 4 G 4

RESULT 37
EFG_CLOPA
ID EFG_CLOPA STANDARD PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 1 K 1

RESULT 38

ES1_RAT
ID ES1_RAT STANDARD PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE ES1 protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
CC P2) is: 8.9, its MW is: 25 kDa.
CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 R 6
|
Db 1 R 1

RESULT 39

FAR6_PENMO
ID FAR6_PENMO STANDARD PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 G 9
|
Db 2 G 2

RESULT 40
FAR9_CALVO
ID FAR9_CALVO STANDARD; PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 9.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; I41978; I41978.
KW Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 1 S 1

RESULT 41
HS70_PINPS
ID HS70_PINPS STANDARD; PRT; 11 AA.
AC P81672;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N164) is: 5.4, its MW is: 73 kDa.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 A 1
|
Db 5 A 5

RESULT 42
LADD_ONCMY
ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jenseuis J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -!-- FUNCTION: Lectin that binds sepharose.
CC -!-- COFACTOR: Calcium is essential for sepharose binding.
CC -!-- SUBUNIT: Multimeric.
KW Lectin; Calcium.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 43
LPW_THETH
ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!-- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X07744; CAA30565.1; -.

KW Tryptophan biosynthesis; Leader peptide.

SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 44

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.

AC P04428;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Leucosulfakinin-I (LSK-I).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberidae; Leucophaea.

OX NCBI_TaxID=6988;

RN [1]

RP SEQUENCE.

RX MEDLINE=86315858; PubMed=3749893;

RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;

RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to

gastrin and cholecystokinin.";

RL Science 234:71-73(1986).

CC -!- FUNCTION: Change the frequency and amplitude of contractions of
the hingut. Inhibits muscle contraction of hindgut.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; A01622; GMROL.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Hormone; Amidation; Sulfation.

FT MOD_RES 6 6 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 2 Q 2

RESULT 45

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.

AC P36885;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Perisulfakinin (Pea-SK-I).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;

OC Blattidae; Periplaneta.

OX NCBI_TaxID=6978;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=90137190; PubMed=2615921;

RA Veenstra J.A.;

RT "Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.";

RL Neuropeptides 14:145-149(1989).

CC --!- FUNCTION: Stimulates hindgut contractions.

CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; A60656; A60656.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Hormone; Amidation; Sulfation.

FT MOD_RES 6 6 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 2 Q 2

RESULT 46

MHBI_KLEPN

ID MHBI_KLEPN STANDARD; PRT; 11 AA.

AC P80580;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).

GN MHBI.

OS Klebsiella pneumoniae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.

OX NCBI_TaxID=573;

RN [1]

RP SEQUENCE.

RX MEDLINE=96349117; PubMed=8760924;

RA Robson N.D., Parrott S., Cooper R.A.;

RT "In vitro formation of a catabolic plasmid carrying Klebsiella pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-hydroxybenzoate.";
RL Microbiology 142:2115-2120(1996).
CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
KW Isomerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 2 K 2

RESULT 47
MLG_THETS
ID MLG_THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Wattez C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum.";
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: Belongs to the POMC family.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 R 6
|
Db 7 R 7

RESULT 48
MORN_HUMAN
ID MORN_HUMAN STANDARD; PRT; 11 AA.

AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
CC in the G2/mitosis transition.
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
CC and was called head activator by the authors, because it induced
CC head-specific growth and differentiation in this animal. It has
CC been found in mammalian intestine and hypothalamus.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 49

NUHM_CANFA
ID NUHM_CANFA STANDARD PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro; IPRO02023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 G 9
|
Db 1 G 1

RESULT 50
 PQQC_PSEFL
 ID PQQC_PSEFL STANDARD; PRT; 11 AA.
 AC P55173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
 biosynthesis protein C) (Fragment).
 GN PQQC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqC family.
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 CC -----
 DR EMBL; X87299; CAA60734.1; -.
 DR PIR; S58244; S58244.
 DR HAMAP; MF_00654; -; 1.
 KW PQQ biosynthesis.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;
 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 P 10
 |
 Db 5 P 5

RESULT 51
 RANC_RANPI
 ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
CC family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 3 P 3

RESULT 52
RE41_LITRU
ID RE41_LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).

CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 G 9
|
Db 1 G 1

RESULT 53
RRPL_CHAV
ID RRPL_CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein) (Fragment).
GN L.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299473; PubMed=2741347;
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC PARAMYXOVIRUSES.
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CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 P 10
|
Db 5 P 5

RESULT 54

RS30_ONCMY

ID RS30_ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O., Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow trout skin.";
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive bacteria.
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 1 K 1

RESULT 55

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.

AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvulI (EC 3.1.21.4) (Endonuclease PvulI)
(R.PvulI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvulI restriction and
RT modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvulI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.18; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 S 2
|
Db 2 S 2

RESULT 56
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerinin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana tigerina*.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic.
 FT DISULFID 3 11
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 R 6
 |
 Db 1 R 1

RESULT 57
 TKC2_CALVO
 ID TKC2_CALVO STANDARD; PRT; 11 AA.
 AC P41518;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin II.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, *Calliphora vomitoria*, that have resemblances to
 RT tachykinins.";
 RL Peptides 15:761-768(1994).
 CC -!- FUNCTION: Myoactive peptide.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 G 9
|
Db 1 G 1

RESULT 58
TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B60409; B60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
 |
Db 1 Q 1

RESULT 59

TKN1_UPERU

ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Endean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.18; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
 |
Db 1 Q 1

RESULT 60

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; C60409; C60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3 Q 3
Db	1 Q 1

RESULT 61
 TKN3_PSEGU
 ID TKN3_PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D60409; D60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 62
TKN4_PSEGU
ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog *Pseudophryne guntheri*";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; E60409; E60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3 Q 3
Db	1 Q 1

RESULT 63
 TKN5_PSEGU
 ID TKN5_PSEGU STANDARD; PRT; 11 AA.
 AC P42990;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide II (PG-SPII).
 OS *Pseudophryne guentheri* (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; *Pseudophryne*.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog *Pseudophryne guntheri*";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth

CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 1 Q 1

RESULT 64
TKNA_HORSE
ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Equus caballus (Horse), and
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN [1]
RP SEQUENCE.
RC SPECIES=Horse;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.porcellus;
RX MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 R 6
|
Db 1 R 1

RESULT 65
TKNA_RANCA
ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A61033; A61033.

DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 1 K 1

RESULT 66
TKNA_RANRI
ID TKNA_RANRI STANDARD PRT; 11 AA.
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranakinin (Substance-P-related peptide).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 1 K 1

RESULT 67

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachtykinin D (RTK D).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!-- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!-- SUBCELLULAR LOCATION: Secreted.
CC -!-- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D61033; D61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 1 K 1

RESULT 68

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
 AC P01293;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musky octopus) (Ozaena moschata), and
 OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoeloidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RT "The isolation and amino acid sequence of eledoisin, the active
 endecapeptide of the posterior salivary glands of Eledone.";
 RL Arch. Biochem. Biophys. 101:56-65(1963).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01561; EOOC.
 DR PIR; B01561; EOOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3 Q 3
Db	1 Q 1

RESULT 69
 UF05_MOUSE
 ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P38643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 48 kDa.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5
|
Db 1 K 1

RESULT 70
ULAG_HUMAN
ID ULAG_HUMAN STANDARD; PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 34 kDa.
DR SWISS-2DPAGE; P31933; HUMAN.
DR Siena-2DPAGE; P31933; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3
|
Db 3 Q 3

Search completed: April 8, 2004, 15:47:22
Job time : 6.15385 secs